

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:35:53 ; Search time 962.98 seconds
(without alignments)
1471.172 Million cell updates/sec

Title: US-08-700-737-11

Perfect score: 396
Sequence: 1 ATGAGTTGCTGTAGCT.....GACCAAGCTGGAATPAAA 396

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl:*
1: gb_bal:*
2: gb_bal2:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_ph:*
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39: gb_pl2:*
40: gb_pl2:*
41: gb_pl2:*
42: gb_pl2:*
43: gb_pl2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Score Match Length DB ID Description

1	375.2	94.7	396	13	MMU16688	U16688 Mus musculus
2	356.2	89.9	396	13	MUSIGKBN	M15814 Mouse Ig ac
3	331.2	83.6	339	13	MUSIGKCOL	M24275 Mouse Ig ge
4	323.2	81.6	805	13	MUSIGKIDAH	L12156 M3129, Mus
5	320	80.8	336	13	MUSIGK2AK	X74588 M. musculus
6	319.8	80.8	323	13	MUSIGKAPD	M64152 Mus musculus
7	319.8	80.8	323	13	MUSIGKAFM	M64161 Mus musculus
8	318.4	80.4	387	13	HS001812	AJ001812 Mus muscu
9	318.4	80.4	339	13	MUSIGKCOI	M24272 Mouse Ig ge
10	318.4	80.4	339	13	MUSIGKCOK	M24274 Mouse Ig ge
11	318.2	80.4	351	13	MMU22904	U22904 Mus musculu
12	305.2	77.1	404	13	RATIGCD2L	M87786 Rat (hybrid
13	303.8	76.7	342	13	MMBV1613L	X53642 M.musculus
14	301.2	76.1	538	13	MMIGVK	X00045 Mouse mRNA
15	300.6	75.9	538	13	MUSIGKAT	R00709 Mouse Ig ka
16	298.4	75.4	417	13	MMU62051	U62051 Mus musculu
17	298	75.3	333	13	MMU01885	U01885 Mus musculu
18	297.6	75.2	342	13	AF003287	AF003287 Mus muscu
19	293.6	74.1	394	6	AR022585	AR022585 Sequence
20	293.6	74.1	393	13	AF045491	AF045491 Mus muscu
21	293.6	74.1	436	13	MMU012556	U012556 Mus muscu
22	293.6	74.1	416	13	MUSIGKCLL	M20828 Mouse IgG2a
23	293.6	74.1	426	13	MUSIGVK	M5313 Mouse Igk p
24	293.6	74.1	394	13	S67233	S67233 IgG3V-muc1
25	293.6	74.1	456	13	MMU39901	U39901 Mus musculu
26	290.4	73.3	393	13	AF013576	AF013576 Mus muscu
27	290.4	73.3	393	13	MUSIGK324A	M32382 Mus musculu
28	288.8	72.9	393	13	MUSIGK514	L39088 Mus musculu
29	288.8	72.9	393	13	MUSIGK940A	L39104 Mus musculu
30	288.8	72.9	393	13	MUSIGK1240	M32384 Mus musculu
31	287.2	72.5	394	6	AR022571	AR022571 Sequence
32	287.2	72.5	393	13	AF045490	AF045490 Mus muscu
33	287.2	72.5	393	13	MUSIGK13A	L39105 Mus musculu
34	286	72.2	384	6	AR013851	AR013851 Sequence
35	285.6	72.1	393	13	AF045494	AF045494 Mus muscu
36	285.6	72.1	393	13	MUSIGK4420	L39087 Mus musculu
37	285.6	72.1	393	13	MUSIGK1025	M32381 Mus musculu
38	285.6	72.1	432	13	MMU62054	U62054 Mus musculu
39	285.6	72.1	956	13	MMKAPLI	X87231 M. musculus
40	284	71.7	427	6	A25561	A25561 H.sapiens B
41	284	71.7	434	6	A25576	A25576 M.musculus
42	284	71.7	434	6	I26965	I26965 Sequence 4
43	284	71.7	427	6	I26967	I26967 Sequence 8
44	284	71.7	420	13	MMU84ILEV	X65775 M.musculus
45	282.4	71.3	394	6	AR022601	AR022601 Sequence

ALIGNMENTS

RESULT 1
LOCUS MMU16688 396 bp mRNA
DEFINITION Mus musculus Ig light chain leader and variable region VK II gene
ACCESSION U16688
NID g1041798
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 396)
AUTHORS White,K.D., Frank,M.B., Foundling,S. and Waxman,F.J.
TITLE Effect of Immunoglobulin variable region structure on C3b and C4b
deposition
JOURNAL Mol. Immunol. 33 (9), 759-768 (1996)
MEDLINE 96406984
REFERENCE 2 (bases 1 to 396)
AUTHORS Frank,B.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology

NID 9197085
KEYWORDS C-region; J-region; germline; immunoglobulin light chain;
SOURCE immunoglobulin-kappa variable region; processed gene.
ORGANISM Mus musculus (clone 36.1.2D) mRNA.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euteria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Matsuda, T. and Kabat, E.A.
TITLE Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1----6)dextran
JOURNAL J. Immunol. 142 (3), 863-870 (1989)
MEDLINE 89110062
FEATURES
source
1..339
location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="36.1.2D"
<1..>339
/note="Ig kappa-chain (V-J2)"
/codon_start=1
/db_xref="PID:g197086"
/translation="DVAVTQPLSPVFDQVSISSRSSQSIANSYNTYLSWYLRK PGSPOLLIGISRFSGVDPDRSGSGSDTFIKISTIRPEDIGMYICQSTHOPYT FGGGTKEIR"
BASE COUNT 87 a 80 c 84 g 88 t
ORIGIN

Query Match 83.6%; Score 331.2; DB 13; Length 339;
Best Local Similarity 99.1%; Pred. No. 1.1e-97;
Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 GATGTTGGTGATCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 120
DB 1 GATGTTGGTGATCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGCAGCTAGTCAGACAGTCTTGCAGAAAGTTTGGGAACCACTATTGGCTTG 180
DB 61 ATCTCTGCAGCTAGTCAGACAGTCTTGCAGAAAGTTTGGGAACCACTATTGGCTTG 120
QY 181 TACCTGCACAGCCTGGCAGTCTCCACAGCTCCATATGAGATTCCACAGATT 240
DB 121 TACCTGCACAGCCTGGCAGTCTCCACAGCTCCATATGAGATTCCACAGATT 180
QY 241 TCTGGGGTCCAGACAGGTTCAAGTGGCAGTTCAGGGACAGATTTCACACTCAAGATC 300
DB 181 TCTGGGGTCCAGACAGGTTCAAGTGGCAGTTCAGGGACAGATTTCACACTCAAGATC 240
QY 301 AGCACAATTAAGCCTGAGAGTGGGATGTTACTACATCAAGAGTACATCAGCCG 360
DB 241 AGCACAATTAAGCCTGAGAGTGGGATGTTACTACATCAAGAGTACATCAGCCG 300
QY 361 TACACGTTCCGAGGGGGACCAAGCTGGAATATAAA 396
DB 301 TACACGTTCCGAGGGGGACCAAGCTGGAATATAAA 336

RESULT 4
MUSIGKIDAH 805 bp DNA ROD 18-JUL-1994
LOCUS W3129; Mus musculus Igk (W3129) chain gene with insertion/deletion mutations.
DEFINITION
ACCESSION U12156
NID g197336
KEYWORDS immunoglobulin kappa-chain; immunoglobulin light chain.
SOURCE Mus musculus (strain BALB/c) DNA.
ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euteria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 805)
AUTHORS Chou, C.L. and Morrison, S.L.
TITLE Intronic sequences determine the expression of kappa light chain genes
JOURNAL Mol. Immunol. 31 (2), 99-107 (1994)
MEDLINE 94142762
REFERENCE 2 (bases 1 to 805)
AUTHORS Chou, C.L. and Morrison, S.L.
TITLE A common sequence motif near nonhomologous recombination breakpoints involving Ig sequences
JOURNAL J. Immunol. 150 (12), 5350-5360 (1993)
MEDLINE 93294290
REFERENCE 3 (bases 1 to 805)
AUTHORS Chou, C.L. and Morrison, S.L.
TITLE An insertion-deletion event in murine immunoglobulin kappa gene resembles mutations at heavy-chain disease loci
JOURNAL Somat. Cell Mol. Genet. 19 (2), 131-139 (1993)
MEDLINE 93289445
FEATURES
source
1..805
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/organism="Mus musculus"
/sub_species="domesticus"
/db_xref="taxon:10090"
/issue_type="myeloma"
join(1..49,456..466)
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/label=leader
1..466
/gene="Igk"
48..55
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/note="putative splice donor sequence"
50..455
/gene="Igk"
145..146
/note="cryptic splice acceptor site in cell line 5S"
/citation=[1]
152..153
/gene="Igk"
/note="deletion breakpoint site in cell line 5S"
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275..276
/gene="Igk"
/note="cryptic splice acceptor in cell line R15"
/citation=[3]
294..313
/gene="Igk"
/note="deleted in cell line R15"
/citation=[3]
/citation=[1]
436..455
/gene="Igk"
/note="putative splice acceptor sequence"
467..805
/gene="immunoglobulin kappa variable region"
/label=V-kappa
467..805
/gene="immunoglobulin kappa variable region"
537..538
/gene="immunoglobulin kappa variable region"
/note="cryptic splice acceptor site, used in cell lines R15, 5S"
/citation=[1]
628..781
/gene="immunoglobulin kappa variable region"
/note="sequences deleted in cell line 5S"
/citation=[2]
BASE COUNT 220 a 158 c 185 g 242 t
ORIGIN

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Query Match      81.6%; Score 333.2; DB 13; Length 805;
Best Local Similarity 93.6%; Pred. No. 5e-95;
Matches 337; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

37 TTTCTGATTCCTGTTCCGGAGTGTGTTGGTGTACACCAACCTCCCTCCCT 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
443 TTCAATTATTGACCTCCAGAGGTGATGTGTGTACCAACCTCCCTCCCT 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  GTACAGCTTTGAGATCAAGTTCTATCTGTGAGGTCTAGTCAGATTTGCAAGAGT 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  503 GTACAGCTTTGAGATCAAGTTCTATCTGTGAGGTCTAGTCAGATTTGCAAGAGT 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  157 TATGGACACCTATTGTCTGTGTGACCTGCACACAGCTGCCAGTCTCCACAGCTCTC 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  563 CATGGATCACCTATTGTCTGTGTGACCTGCACACAGCTGCCAGTCTCCACAGCTCTC 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  217 ATCTATGGATTTCCACAGATTTTCTGGGGTCCAGACAGTCTGAGTGGCTTCA 276
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  623 ATCTATGGATTTCCACAGATTTTCTGGGGTCCAGACAGTCTGAGTGGCTTCA 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  277 GGGACAGATTTCCACACTCAAGATCAACACATTAAGCTTGAGACTTGGAAATGTATTAC 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  683 GGGACAGATTTCCACACTCAAGATCAACACATTAAGCTTGAGACTTGGAAATGTATTAC 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  337 TCGTTTCAAGGTACACATGACCGGTACACGTTCCGAGGGGGACCAAGCTTGGAAATTA 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  743 TCGTTTCAAGGTACACATGACCGGTACACGTTCCGAGGGGGACCAAGCTTGGAAATTA 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
MUSIG2AK      336 bp      RNA      ROD      20-SEP-1993
DEFINITION M.musculus Ig92a kappa chain variable region (antibody MCA75).
ACCESSION X74588
NID 9402597
KEYWORDS Ighv gene; immunoglobulin; immunoglobulin variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Fischer, R.
JOURNAL Direct Submission
Submitted (16-AUG-1993) R. Fischer, Botanical Inst. (RWTH Aachen,
Biology I), Worringer Weg 1, 52074 Aachen, FRG
2 (bases 1 to 336)
AUTHORS Fischer, R., Voss, A., Hunziker, W., Stierhof, Y.D. and Kreuzaler, F.
TITLE Production and cloning of TMV-specific monoclonal antibodies
JOURNAL Unpublished
FEATURES
Location/Qualifiers
1..336
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/dev_stage="16 weeks old"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="(X63-Ag8.653 X BALB/c spleen)"
/clone_id="puc18"
/clone_cdna="L75"
1..336
V_region
/gene="IGLV75"
/note="variable region IGLV75"
1..336
misc_feature
/gene="IGLV75"
1..69
/gene="IGLV75"
/note="FRW I region IGLV75"
1..336
CDS
/note="IGLV75"
/note="protein sequence is in conflict with the conceptual
translation."

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PGQSPQLIIGISNRSFSGVDPDRSGSGSIDFTIKITISDGLMGTTCIGTHQPTT
FGACTRIELK"
70..117
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/note="CDR I region IGLV75"
118..162
misc_feature
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/note="FRW II region IGLV75"
163..183
misc_feature
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184..279
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/gene="IGLV75"
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/note="CDR III region IGLV75"
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ORIGIN

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Best Local Similarity 97.0%; Pred. No. 4.9e-94;
Matches 326; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY  61 GATGTGTGAGTCACTCAACTCCACTCCCTGCTGACAGTTGGAGATCAAGTTCT 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  1 GATGTGTGAGTCACTCAACTCCACTCCCTGCTGACAGTTGGAGATCAAGTTCT 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  121 ATCTCTGAGGTCTAGTCAAGTCTTGCAAAGATTTGGAACACCTATTGTCTTGG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  61 ATCTCTGAGGTCTAGTCAAGTCTTGCAAAGATTTGGAACACCTATTGTCTTGG 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  181 TACCTGCACACAGCTGGCCAGTCTCCACAGCTCCTCACTATGAGATTCCACAGATT 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  121 TACCTGCACACAGCTGGCCAGTCTCCACAGCTCCTCACTATGAGATTCCACAGATT 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  241 TCTGGGGTGGCCGACAGGTTCAGTGGAGTGGTTCAGGAGAGATTTCACACTCAAGATC 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  181 TCTGGGGTGGCCGACAGGTTCAGTGGAGTGGTTCAGGAGAGATTTCACACTCAAGATC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  301 AGCACAATAAAGCTTGAGACTTGGGAATGTATTACTGTTACAGAGTACACATCAGCCG 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  241 AGCACAATAAAGCTTGAGAGACTTGGGAATGTATTACTGTTACAGAGTACACATCAGCCG 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  361 TACAGCTTCGAGAGGGGGACCAAGCTGCAATTA 396
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB  301 TACAGCTTCGAGAGGGGGACCAAGCTGCAATTA 336
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
MUSIGKAPD      333 bp      mRNA      ROD      13-JUN-1996
DEFINITION Mus musculus Ig active kappa-chain mRNA V-region.
ACCESSION M64152
NID 9196688
KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 323)
AUTHORS Caton, A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and

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TITLE Gerhard W.
 Many variable region genes are utilized in the antibody response of BALB/c mice to the influenza virus A/PR/8/34 hemagglutinin
 JOURNAL J. Immunol. 147 (5), 1675-1686 (1991)
 MEDLINE 91349593
 COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.
 FEATURES Location/Qualifiers
 Source 1..323
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 /strain="BALB/c"
 /sub_species="domesticus"
 /db_xref="taxon:10090"
 /cell_line="H140-IE6"
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 /codon_start=1
 /product="immunoglobulin kappa-chain VK-1"
 /db_xref="PID:9554083"
 /translation="DVVVTQPLPLPSFGDQVSISSRSGSLANSYNTLYSLYLR PGOSPOLIYGISNRFSGVDPDRFSGSSGIDFTLKISTINPEDLGMYYCLOGTHQPYT FGGGT"
 BASE COUNT 78 a 79 c 79 g 87 t
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 Query Match 80.8%; Score 319.8; DB 13; Length 323;
 Best Local Similarity 99.4%; Pred. No. 5.7e-94;
 Matches 321; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 61 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 120
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 Db 1 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 60
 Oy 121 ATCTCTGAGGCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACCTATTGTCTGG 180
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 Db 61 ATCTCTGAGGCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACCTATTGTCTGG 120
 Oy 181 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCAAAGATT 240
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 Db 121 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCAAAGATT 180
 Oy 241 TCTGGGGTCCAGACAGGTTCAAGTGGCAAGTTCAGGAGACATTTCACTCAAGATC 300
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 Db 181 TCTGGGGTCCAGACAGGTTCAAGTGGCAAGTTCAGGAGACATTTCACTCAAGATC 240
 Oy 301 AGCAATTAAGCCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATACAGCC 360
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 Db 241 AGCAATTAAGCCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATACAGCC 300
 Oy 361 TACAGTTCCGAGGGGGACCAA 383
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 Db 301 TACAGTTCCGAGGGGGACCAA 323
 RESULT 7
 MUSIGRAF 323 bp mRNA ROD 13-JUN-1996
 LOCUS Mus musculus Ig active kappa-chain mRNA V-region.
 DEFINITION M64161
 ACCESSION 9196706
 NID
 KEYWORDS V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 323)
 AUTHORS Gerzon, A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and Gerhard, W.
 TITLE Many variable region genes are utilized in the antibody response of BALB/c mice to the influenza virus A/PR/8/34 hemagglutinin
 JOURNAL J. Immunol. 147 (5), 1675-1686 (1991)

MEDLINE 91349593
 COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.
 FEATURES Location/Qualifiers
 Source 1..323
 /organism="Mus musculus"
 /strain="BALB/c"
 /sub_species="domesticus"
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 /translation="DVVVTQPLPLPSFGDQVSISSRSGSLANSYNTLYSLYLR PGOSPOLIYGISNRFSGVDPDRFSGSSGIDFTLKISTINPEDLGMYYCLOGTHQPYT FGGGT"
 BASE COUNT 78 a 79 c 79 g 87 t
 ORIGIN
 Query Match 80.8%; Score 319.8; DB 13; Length 323;
 Best Local Similarity 99.4%; Pred. No. 5.7e-94;
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 Oy 61 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 120
 |||||
 Db 1 GATGTTGGTGACACCAACTCCACTCTCCCTGCTGACGTTGGAGATCAAGTTCT 60
 Oy 121 ATCTCTGAGGCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACCTATTGTCTGG 180
 |||||
 Db 61 ATCTCTGAGGCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACCTATTGTCTGG 120
 Oy 181 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCAAAGATT 240
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 Db 121 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCTCATCTATGGGATTTCCAAAGATT 180
 Oy 241 TCTGGGGTCCAGACAGGTTCAAGTGGCAAGTTCAGGAGACATTTCACTCAAGATC 300
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 Db 181 TCTGGGGTCCAGACAGGTTCAAGTGGCAAGTTCAGGAGACATTTCACTCAAGATC 240
 Oy 301 AGCAATTAAGCCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATACAGCC 360
 |||||
 Db 241 AGCAATTAAGCCTGAGGACTTGGGAATGATTAAGTCTTCAAGTTCACATACAGCC 300
 Oy 361 TACAGTTCCGAGGGGGACCAA 383
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 Db 301 TACAGTTCCGAGGGGGACCAA 323
 RESULT 8
 HS001812 387 bp mRNA ROD 30-MAR-1998
 LOCUS Mus musculus partial mRNA sequence for immunoglobulin light chain V-region (clone 2C7/K18F).
 DEFINITION AJ001812
 ACCESSION G3004453
 NID
 KEYWORDS immunoglobulin; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 387)
 AUTHORS McElveen, J., Clark, M.R., Smith, S.J., Sewell, H.F. and Shakhb, F.
 TITLE Primary sequence and molecular model of the variable region of a mouse monoclonal anti-der P I antibody showing the same epitope specificity as human 19E: Production of a mouse monoclonal anti-idiotypic that recognises a cross-reactive idiotypic on human 19E
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 387)
 AUTHORS Clark, M.R.
 TITLE Direct Submission

JOURNAL Submitted (27-SEP-1997) Clark M.R., Pathology Department,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK.
FEATURES Location/Qualifiers
source 1. 387
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/rearranged
/cell_line="2C7"
/cell_type="hybridoma"
/clone="12C7/K18P"
/tissue_type="B-cell hybridoma"
<1..>387
/codon_start=1
/evidence=experimental
/product="variable region of Ige light chain"
/db_xref="pid:c1284813"
/db_xref="pid:g3004454"
/translation="DYVMQTPLSPVPSFGDOVISICSSQSLSANSYNTLYSWYLHK
PGQSPQLITIGISIDRFSGVDPFSGSGSDFTLKISTIKPEDLGMTCLOCTHQPWT
FGGTRLEIKRADAAPTVSIFFPSSSQ"
BASE COUNT 96 a 100 c 91 g 100 t
ORIGIN
Query Match 80.4%; Score 318.4; DB 13; Length 387;
Best Local Similarity 96.7%; Pred. No. 1.7e-93;
Matches 325; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 61 GATGTTGCTGACTCAACTCCACTCTCCCTGCTGACGCTTTGGAGATCAAGTTCT 120
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DB 1 GATGTTTGTATGACCCAACTCCACTCTCCCTGCTGACGCTTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGAGGCTCTAGTCAGAGCTTGCAGAGTTATGAGGAACCTATTGTCTTG 180
|||||
DB 61 ATCTCTGAGGCTCTAGTCAGAGCTTGCAGAGTTATGAGGAACCTATTGTCTTG 120
QY 181 TACCTGCACAAAGCCTGGCAGTCTCCACAGCTCTCATCTATGAGATTGCCAAGATT 240
|||||
DB 121 TACCTGCACAAAGCCTGGCAGTCTCCACAGCTCTCATCTATGAGATTGCCAAGATT 180
QY 241 TCTGGGGTGCACAGAGTTCAGTGGCAGTGGTTCAGAGGACATTTTCACATCAAGATC 300
|||||
DB 181 TCTGGGGTGCACAGAGTTCAGTGGCAGTGGTTCAGAGGACATTTTCACATCAAGATC 240
QY 301 AGCACATATAAGCCTGAGAGCTTGGGATGTATTACTGCTTACAGGTACACATCAGCCG 360
|||||
DB 241 AGCACATATAAGCCTGAGAGCTTGGGATGTATTACTGCTTACAGGTACACATCAGCCG 300
QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAAATATAA 396
|||||
DB 301 TGGACGTTGCGTGGAGGACCAAGCTGGAAATATAA 336
RESULT 9
MUSIGKCOI 339 bp mRNA ROD 07-MAR-1995
LOCUS Mouse Ig germline X24 kappa-chain mRNA (V-J1), partial cds.
DEFINITION M24272
ACCESSION
KEYWORDS
C-region; J-region; germline; immunoglobulin light chain;
immunoglobulin-kappa variable region; processed gene.
SOURCE Mus musculus (clone 16.4.12P) mRNA.
ORGANISM Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognath; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Matsuda,T. and Kabat,E.A.
TITLE Variable region cDNA sequences and antigen binding specificity of
mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled
to proteins. T-dependent analogues of alpha(1---6)dextran
J. Immunol. 142 (3), 863-870 (1989)
JOURNAL

MEDLINE 89110062
FEATURES Location/Qualifiers
source 1. 339
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="16.4.12P"
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/note="Ig kappa-chain (V-J1)"
/codon_start=1
/db_xref="pid:g197080"
/translation="DYVMQTPLSPVPSFGDOVISICSSQSLSANSYNTLYSWYLHK
PGQSPQLITIGISIDRFSGVDPFSGSGSDFTLKISTIKPEDLGMTCLOCTHQPWT
FGGTRLEIKRADAAPTVSIFFPSSSQ"
BASE COUNT 86 a 81 c 84 g 88 t
ORIGIN
Query Match 80.4%; Score 318.4; DB 13; Length 339;
Best Local Similarity 96.7%; Pred. No. 1.6e-93;
Matches 325; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 61 GATGTTGCTGACTCAACTCCACTCTCCCTGCTGACGCTTTGGAGATCAAGTTCT 120
|||||
DB 1 GATGTTGCTGACTCAACTCCACTCTCCCTGCTGACGCTTTGGAGATCAAGTTCT 60
QY 121 ATCTCTGAGGCTCTAGTCAGAGCTTGCAGAGTTATGAGGAACCTATTGTCTTG 180
|||||
DB 61 ATCTCTGAGGCTCTAGTCAGAGCTTGCAGAGTTATGAGGAACCTATTGTCTTG 120
QY 181 TACCTGCACAAAGCCTGGCAGTCTCCACAGCTCTCATCTATGAGATTGCCAAGATT 240
|||||
DB 121 TACCTGCACAAAGCCTGGCAGTCTCCACAGCTCTCATCTATGAGATTGCCAAGATT 180
QY 241 TCTGGGGTGCACAGAGTTCAGTGGCAGTGGTTCAGAGGACATTTTCACATCAAGATC 300
|||||
DB 181 TCTGGGGTGCACAGAGTTCAGTGGCAGTGGTTCAGAGGACATTTTCACATCAAGATC 240
QY 301 AGCACATATAAGCCTGAGAGCTTGGGATGTATTACTGCTTACAGGTACACATCAGCCG 360
|||||
DB 241 AGCACATATAAGCCTGAGAGCTTGGGATGTATTACTGCTTACAGGTACACATCAGCCG 300
QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAAATATAA 396
|||||
DB 301 TGGACGTTGCGTGGAGGACCAAGCTGGAAATATAA 336
RESULT 10
MUSIGKCOI 339 bp mRNA ROD 07-MAR-1995
LOCUS Mouse Ig germline J558 kappa-chain mRNA (V-J4), partial cds.
DEFINITION M24274
ACCESSION
KEYWORDS
C-region; J-region; germline; immunoglobulin light chain;
immunoglobulin-kappa variable region; processed gene.
SOURCE Mus musculus (clone 35.8.2H) mRNA.
ORGANISM Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognath; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Matsuda,T. and Kabat,E.A.
TITLE Variable region cDNA sequences and antigen binding specificity of
mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled
to proteins. T-dependent analogues of alpha(1---6)dextran
J. Immunol. 142 (3), 863-870 (1989)
JOURNAL
MEDLINE 89110062
FEATURES Location/Qualifiers
source 1. 339
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="35.8.2H"
<1..>339
/note="Ig kappa-chain (V-J4)"
CDS

/codon_start=1
/db_xref="PID:g197084"
/translation="DVTYOTPLPSFGDOVISCSQSILVKSQDNTLSWLRK
PGSPOLLIVGISNRFSGVDPDRFSGSGSGDTFLIKSTIKPEDLGMVYCLQGTHQPMV
FGSGTKLEIKR"
BASE COUNT 86 a 81 c 84 g 88 t
ORIGIN

Query Match 80.4%; Score 318.4; DB 13; Length 339;
Best Local Similarity 96.7%; Pred. No. 1.6e-93;
Matches 325; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 61 GATGTTGGTGAACAACTCCACTCTCCCTGCTGAGCTTGGAGATCAAGTTCT 120
DB 1 GATGTTGGTGAACAACTCCACTCTCCCTGCTGAGCTTGGAGATCAAGTTCT 60
QY 121 ATCTTTGAGAGTCTAGTCAGAGTCTTGCAAGAGTTATGGACACCTATTGCTTGG 180
DB 61 ATCTTTGAGAGTCTAGTCAGAGTCTTGCAAGAGTTATGGACACCTATTGCTTGG 120
QY 181 TACCGCAAGAGCTGGCCAGTCTCCACAGCTCATCATATGAGATTGCCAAGATT 240
DB 121 TACCGCAAGAGCTGGCCAGTCTCCACAGCTCATCATATGAGATTGCCAAGATT 180
QY 241 TCTGGGGTGCAGACAGGTTTCAGTGGCAGTGGTTCAGGACAGATTTCACACTCAAGATC 300
DB 181 TCTGGGGTGCAGACAGGTTTCAGTGGCAGTGGTTCAGGACAGATTTCACACTCAAGATC 240
QY 301 AGCACAATAAAGCTTGAGAGCTTGGGAATGTATCTGCTTACAGAGTACATCAGCCG 360
DB 241 AGCACAATAAAGCTTGAGAGCTTGGGAATGTATCTGCTTACAGAGTACATCAGCCG 300
QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAAATAAAA 396
DB 301 TGGACGTTGGGTGGAGGACCAACTGGAAATCAAA 336

RESULT 11

MMU22904 351 bp mRNA ROD 24-OCT-1996
LOCUS Mus musculus anti-human interferon-gamma receptor monoclonal
DEFINITION antibody gammaR99, IgG V κ region mRNA, partial cds.
ACCESSION U22904
KEYWORDS 9727380

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 351)
AUTHORS Bridges,A., Birch,A., Williams,G., Aguet,M., Schlatter,D.,
Huber,W., Garotta,G., and Robinson,J.A.
TITLE Variable region cDNA sequences and characterization of murine
anti-human interferon gamma receptor monoclonal antibodies that
inhibit receptor binding by interferon gamma
Mol. Immunol. 32 (17-18), 1329-1338 (1995)

REFERENCE 2 (bases 1 to 351)
AUTHORS Bridges,A., Birch,A., Williams,G., Robinson,J.A., Aguet,M.,
Weissman,C. and Garotta,G.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-1995) Ashley Birch, Organic Chemistry Institute,
University of Zurich, Winterthurerstr 133, Zurich, CH-8057,
Switzerland

FEATURES
SOURCE Location/Qualifiers
1..351

/organism="Mus musculus"
/strain="BALB/C"
/note="Mouse hybridoma gammaR99; V κ amplified by PCR and
cloned into M13mp18."
/db_xref="taxon:10090"

primer_bind 1..36
/note="VFPR1C PCR Primer"
CDS <1..351
/codon_start=1
/product="IgG V κ region"
/db_xref="PID:g1727381"
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QPMVFGSGTKLEIKR"
primer_bind 328..351
/note="VFPR4A PCR Primer"

BASE COUNT 89 a 87 c 83 g 92 t
ORIGIN

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Best Local Similarity 94.8%; Pred. No. 1.9e-93;
Matches 329; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 50 TTTCGAGAGTGAATGTGTGAGTCACTCAACTCCACTCTCCCTGCTGAGCTTGGAG 109
DB 2 TATCCATGACAGATATTATGATGACCAACTCCACTCTCCCTGCTGAGCTTGGAG 61
QY 110 ATCAAGTTCTATCTCTTGAGTCTAGTCAAGTCTTGCAAGAGTTATGGAAACACT 169
DB 62 ATCAAGTTCTATCTCTTGAGTCTAGTCAAGTCTTGCAAGAGTTATGGAAACACT 121
QY 170 ATTGCTGTGTACTCTGACCAAGCTGGCCAGTCTCCACACTCTCTATCTATGGATT 229
DB 122 CTGTGCTGTGTACTCTGACCAAGCTGGCCAGTCTCCACACTCTCTATCTATGGATT 181
QY 230 CCAACAGATTCTTGAGGGTGCAGACAGTTCAGTGGCAGTGGTTCAGGACAGATTTC 289
DB 182 CCAACAGATTCTTGAGGGTGCAGACAGTTCAGTGGCAGTGGTTCAGGACAGATTTC 241
QY 290 CACTCAAGATCAGACAAATAAAGCTTGAGACTTGGGAATGTATCTACTGCTTCAAGGTA 349
DB 242 CACTCAAGATCAGACAAATAAAGCTTGAGACTTGGGAATGTATCTACTGCTTCAAGGTA 301
QY 350 CACATCAGCCGTACACGTTCCGAGGGGGACCAAGCTGGAAATAAAA 396
DB 302 CACATCAGCCGTACACGTTCCGAGGGGGACCAAGCTGGAAATAAAA 348

RESULT 12

RATIGCD2L 404 bp mRNA ROD 18-FEB-1993
LOCUS Rat (hybridoma YTH655) immunoglobulin light chain variable region,
DEFINITION complementarity-determining regions mRNA, partial cds.
ACCESSION M87786
KEYWORDS 9204705

SOURCE V-region; complementarity determining region; immunoglobulin; light
chain.
ORGANISM Rattus rattus

REFERENCE 1 (bases 1 to 404)
AUTHORS Shearin,J., Walsh,L., Waldmann,H. and Crowe,J.S.
JOURNAL Unpublished (1992)
TITLE Location/Qualifiers

FEATURES
SOURCE 1..404

5'UTR
CDS
/organism="Rattus rattus"
/db_xref="taxon:10117"
/cell_line="YTH 655(5)6"
/cell_type="hybridoma"
1..17
/partial
/note="putative"
18..404
/partial
/note="Anti-CD2 (T11; LFA-2) variable region; putative"

AUTHORS Schiff, C., Corbet, S., Millili, M. and Fougereau, M.
 TITLE Interstrain conservation of the murine GAT-specific antibody-V-
 kappa repertoire as analyzed at the germline gene level
 JOURNAL EMBO J. 2 (10), 1771-1776 (1983)
 MEDLINE 84057697

COMMENT Data kindly reviewed (09-MAY-1985) by M. Fougereau.
 FEATURES Location/Qualifiers

source

MRNA

/organism="Mus musculus"
 /db_xref="taxon:10090"
 1..>538

sig_peptide

/note="messenger RNA"
 132..188

V_region

/note="signal peptide"
 132..>538

/note="variable region joining segment (538 is 2nd base in
 codon)"
 132..>538

CDS

/note="variable region joining segment (538 is 2nd base in
 codon)"
 /db_xref="pid:g52533"
 /translation="MTLPRLVLMFWIPASXSDVYMTPTSLPYSLADQSLGSR
 SSVSHSNNTLYIMLQKPGSPKLLIRVSNRSGVDRSGSGSGDFLNLISRV
 EAEDGVYCCFQGTHTVPHFGGCTKLDIRADAA"

BASE COUNT 127 a 133 c 132 g 143 t 3 others
 ORIGIN

Query Match 76.1%; Score 301.2; DB 13; Length 538;
 Best Local Similarity 86.6%; Pred. No. 7.2e-88;

Matches 343; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

QY 1 ATGAAGTTCCTGTTAGGCTGTGGCTCTGTTGTTGATGTCCTGTTCCGAGGT 60
 DB 132 ATGAAGTTCCTGTTAGGCTGTGGCTGTGGCTCTGTTGTTGATGTCCTGTTCCGAGGT 188
 QY 61 GATGTTGTGATGATCAAACTCCACTCTCCCTGCTGTCAGTTGGAGATCAAGTTTC 120
 DB 189 GATGTTGTGATGATCAAACTCCACTCTCCCTGCTGTCAGTTGGAGATCAAGTTTC 248
 QY 121 ATCTCTGCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 180
 DB 249 ATCTCTGCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 308
 QY 181 TACCTGCAGAACCTGAGGCTGCTCCAGACCTCTCATCTATGAGATTCCACAGATT 240
 DB 309 TACCTGCAGAACCTGAGGCTGCTCCAGACCTCTCATCTATGAGATTCCACAGATT 368
 QY 241 TCTGGGGTCCAGACAGAGTTGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 369 TCTGGGGTCCAGACAGAGTTGATGATGATGATGATGATGATGATGATGATGATG 428
 QY 301 AGCACATAAAGCTTGAGAGCTTGGAGATGATGATGATGATGATGATGATGATGATG 360
 DB 429 AGCACATAAAGCTTGAGAGCTTGGAGATGATGATGATGATGATGATGATGATGATG 488
 QY 361 TACAGTTGGAGAGGGGACCAAGCTGGAATATAA 396
 DB 489 CACACGTTGGAGAGGGGACCAAGCTGGAATATAA 524

RESULT 15

MUSIGKAT

LOCUS MUSIGKAT 538 bp MRNA ROD 01-MAY-1984
 DEFINITION Mouse Ig kappa active anti-GAT L XIX 27 V-J region mRNA.
 ACCESSION K00709
 NID 9196775

KEYWORDS

C-region: J-region: V-region: complementarity determining region;
 framework region: hypervariable region; immunoglobulin light chain;
 immunoglobulin-kappa; processed gene.
 SOURCE Mouse cDNA to hybridoma 68 Ca 1.7 (BALB/c spleen cells fused with
 myeloma cell line X63 Ag8 653) mRNA, clone L XIX 27.

ORGANISM Mus musculus

Eukaryota; Eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Murimorpha; Muridae;
 Murinae; Mus.

REFERENCE 1 (bases 1 to 538)

AUTHORS Schiff, C., Corbet, S., Millili, M. and Fougereau, M.
 TITLE Interstrain conservation of the murine GAT-specific antibody
 V-kappa repertoire as analysed at the germline level
 JOURNAL EMBO J. 2, 1771-1776 (1983)
 MEDLINE 84057697

FEATURES Location/Qualifiers

source

1..538
 /organism="Mus musculus"
 /db_xref="taxon:10090"

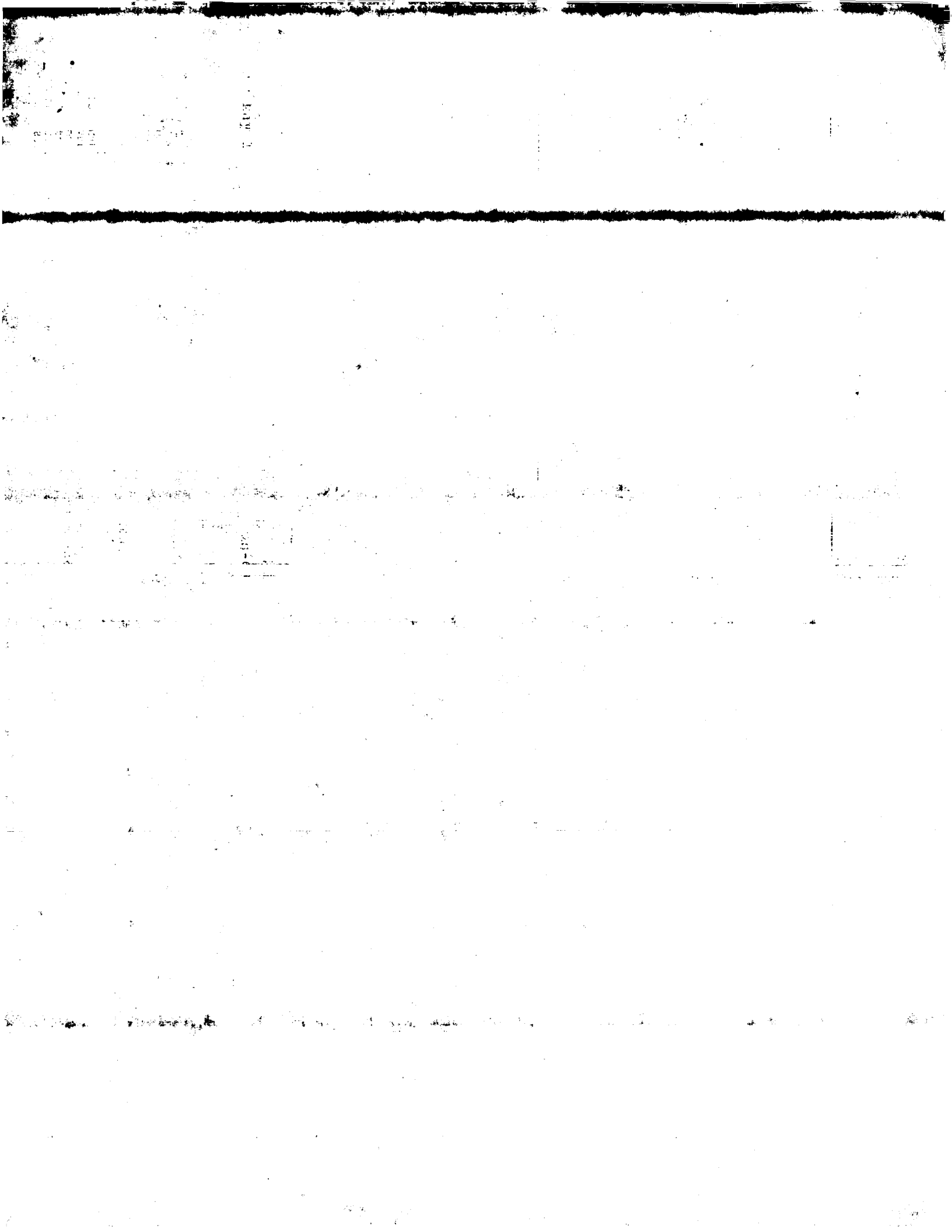
BASE COUNT 127 a 133 c 133 g 143 t 2 others
 ORIGIN

Query Match 75.9%; Score 300.6; DB 13; Length 538;
 Best Local Similarity 86.6%; Pred. No. 1.1e-87;

Matches 343; Conservative 0; Mismatches 50; Indels 3; Gaps 1;

QY 1 ATGAAGTTCCTGTTAGGCTGTGGCTCTGTTGTTGATGTCCTGTTCCGAGGT 60
 DB 132 ATGAAGTTCCTGTTAGGCTGTGGCTGTGGCTCTGTTGTTGATGTCCTGTTCCGAGGT 188
 QY 61 GATGTTGTGATGATCAAACTCCACTCTCCCTGCTGTCAGTTGGAGATCAAGTTTC 120
 DB 189 GATGTTGTGATGATCAAACTCCACTCTCCCTGCTGTCAGTTGGAGATCAAGTTTC 248
 QY 121 ATCTCTGCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 180
 DB 249 ATCTCTGCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 308
 QY 181 TACCTGCAGAACCTGAGGCTGCTCCAGACCTCTCATCTATGAGATTCCACAGATT 240
 DB 309 TACCTGCAGAACCTGAGGCTGCTCCAGACCTCTCATCTATGAGATTCCACAGATT 368
 QY 241 TCTGGGGTCCAGACAGAGTTGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 369 TCTGGGGTCCAGACAGAGTTGATGATGATGATGATGATGATGATGATGATGATG 428
 QY 301 AGCACATAAAGCTTGAGAGCTTGGAGATGATGATGATGATGATGATGATGATGATG 360
 DB 429 AGCACATAAAGCTTGAGAGCTTGGAGATGATGATGATGATGATGATGATGATGATG 488
 QY 361 TACAGTTGGAGAGGGGACCAAGCTGGAATATAA 396
 DB 489 CACACGTTGGAGAGGGGACCAAGCTGGAATATAA 524

Search completed: May 11, 1999, 12:00:26
 Job time: 1473 sec



D6		321	AGCAGATGGAGGCTGAGGATGTTCGGGGTTTATCACTGCATGCAGGCTCTACAAATCCCT	380
OY		361	TACACGTTGGAGGGGGGCCAAGAATTGGAATAAAA	396
D6		381	CACACTTTTGCCAGGGGACCACATGGAGATCAA	416


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RESULT 3
AA464313 363 bp mRNA EST 10-JUN-1997
LOCUS z78c12.r1 Soares ovary tumor NBH0T Homo sapiens cDNA clone 809878
DEFINITION 5' similar to gb:xt2467 IG KAPPA CHAIN PRECURSOR V-II REGION
(HUMAN); mRNA sequence.
ACCESSION AA464313
NID g2189197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
TITLE JOURNAL
COMMENT Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 E7 from Amersham.
FEATURES
source
1..363
location/Qualifiers
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCGAATGAGGAGCGCGCGCTTTTCTTTTCTTTT 3']
TGTACCAATCGAATGAGGAGCGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_lib="Soares ovary tumor NBH0T"
/sex="Female"
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/lab_host="DH10B (ampicillin resistant)"
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BASE COUNT 81 a 94 c 95 g 93 t
ORIGIN
Query Match 52.4%; Score 207.6; DB 20; Length 363;
Best Local Similarity 74.6%; Pred. No. 1,2e-55;
Matches 261; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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Db 185 GTTCTATCGGCGCTCCGGGGTCCCTACAGGTTCAAGTGCAGTGATCAGGCACACATT 244
Qy 287 TCACATCAAGATGACACATTAAGCTGGAGCTGGGAATGATATCTACTACAG 346
Db 245 TTACACTGAAATATGACAGAGTGAAGGCTGAGATGTGGGGTTTATTTACTGATCAG 304
Qy 347 GTACATCAAGCCGTACAGCTTCGAGGGGGAGCCAAAGCTGAATAA 396
Db 305 CTCTCAACCTTATTCAGCTTTCGGCCCTGGAGCAAAAGTATATCAAA 354

RESULT 4
H27034 467 bp mRNA EST 12-JUL-1995
LOCUS y165605.r1 Homo sapiens cDNA clone 163113 5' similar to gb:xt2467
DEFINITION IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);..
ACCESSION H27034
NID 9897024
KEYWORDS EST.
SOURCE human clone-163113 library-Soares breast 3NBHST vector-pT73D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13RPI Rsite1-Not I Rsite2-Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCGAATGAGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adapters (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M. Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Channata; Tetrápoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 467)
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
TITLE JOURNAL
COMMENT Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 352
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source
1..467
location/Qualifiers
/organism="Homo sapiens"
/clone="163113"
BASE COUNT 96 a 122 c 122 g 123 t 4 others
ORIGIN
Query Match 51.2%; Score 202.6; DB 11; Length 467;
Best Local Similarity 74.2%; Pred. No. 4.9e-54;
Matches 256; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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Db 63 GATATGTGATGACTACTCTCCACTCTCCAGCCCGTCACCCCTCGAGAGCCGGCTCC 122
QY 121 ATCTCTTCAGAGTCTAGTACAGAGTCTTCAAGAGTATGGAACACCTATTGTCGG 180
Db 123 ATCTCTTCAGAGTCTAGTACAGAGTCTTCAAGAGTATGGAACACCTATTGTCGG 182
QY 181 TACCTGCAGAACCTGGCCAGTCTCCACAGCTCTCTATCTATGAGATTGCCAAGATT 240
Db 183 TACCTGCAGAACCTGGCCAGTCTCCACAGCTCTCTATCTATGAGATTGCCAAGATT 242
QY 241 TCTGGGGCCAGACAGTCTGAGTGGAGTTCAGGAGAGATTCACACTCAAGATC 300
Db 243 TCCGGGGCCAGACAGTCTGAGTGGAGTTCAGGAGAGATTCACACTCAAGATC 302
QY 301 AGCACAATAAGCCTGAGACTTGGGAATGATTACTGCTTACAA 345
Db 303 AGTAGAGTGAGGCTGAGAGTGTGGCTTTACTCTGATGCA 347

RESULT 5
AA602059 374 bp mRNA EST 08-OCT-1997
LOCUS no95b02.sl NCI-CGAP_P2 Homo sapiens cDNA clone IMAGE:1114539
DEFINITION similar to gb:X55400.cdsl IG KAPPA CHAIN PRECURSOR V-II REGION
(HUMAN); contains Alu repetitive element; mRNA sequence.
ACCESSION AA602059
NID 92435848
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 374)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquil,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.llnl.gov/bdip/image/image.html

Insert Length: 1123 Std Error: 0.00
Seq primer: -40ml3 fwd. Ex from Amersham
High quality sequence stop: 369.

FEATURES

Location/Qualifiers
1..374
/organism="Homo sapiens"
/note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDS-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Kitzman."
/db_xref="taxon:9606"
/clone="IMAGE:1114539"
/clone_1lb="NCI-CGAP_P2"
/sex="Male"
/dev_stage="45 years old"

BASE COUNT 78 a 105 c 102 g 89 t
ORIGIN

Query Match 47.8%; Score 189.2; DB 24; Length 374;
Best Local Similarly 71.7%; Pred. No. 8.1e-50;
Matches 248; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 ATGAAGTGGCTGTAGCTGTGGTCTCTGTTGTTGATTCGATTCGATTCGAGGT 60
Db 29 ATGAGGCTCTCTGCTCAGCTTCTGGGCTGTGATGCTTGGTCCGATTCAGTGG 88
QY 61 GATGTGTGATGACTCAACCTCCACTCTCCCTGCTCAGCTTGGAGATCAAGTTCT 120
Db 89 GATATGTGATGACCCAGACAGCTCCGACCTCTCAGCTTCAACCTTGACAGCGGCTCC 148
QY 121 ATCTCTTCAGAGTCTAGTACAGAGTCTTGGCAAGAGTATGGAACACCTATTGTC 180
Db 149 ATCTCTTCAGAGTCTAGTACAGAGTCTTGGCAAGAGTATGGAACACCTATTGTC 208
QY 181 TACCTGCAGAACCTGGCCAGTCTCCACAGCTCTCTATCTATGAGATTGCCAAGATT 240
Db 209 CTGACACAGAGCCAGCCAGCTCCACAGCTCTATCTATGAGATTGCCAAGATT 268
QY 241 TCTGGGGTCCAGACAGTCTGAGTGGAGTTCAGGAGACAGATTTCACACTCAAGATC 300
Db 269 TCTGGGGTCCAGACAGTCTGAGTGGAGTTCAGGAGACAGATTTCACACTCAAGATC 328
QY 301 AGCACAATAAGCCTGAGACTTGGGAATGATTACTGCTTACAA 346
Db 329 AGTAGAGTGAGGCTGAGAGTGTGGGCTTTACTCTGATGCA 374

RESULT 6
LOCUS T27587 359 bp mRNA EST 06-SEP-1995
DEFINITION EST100475 Homo sapiens cDNA 5' end similar to Immunoglobulin kappa
light chain V region (GB:X63397) (IT:3865).
ACCESSION T27587
NID 9609685
KEYWORDS EST.
SOURCE Human primer-M13 Reverse library-Human Pancreas.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 359)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bull, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chui, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodex, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,
Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T.,
Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudak, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, T., Bednarek, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinko, D., Feng, P., Ferris, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Guber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Miesner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Hasseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Galtherburg, MD 20878

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 335)
Eukaryotae: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria:	
Primates: Catarrhini: Hominoidea: Homo.	
Hillier, L., Allen, M., Bowles, L., Dubouque, T., Gelsel, G., Jost, S.,	
Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Merrit, M., "	

RESULT	10
AA496610	
LOCUS	AA496610 287 bp mRNA EST 12-AUG-1997
DEFINITION	zv338g06.r1 Soares ovary tumor NBH07 Homo sapiens CDNA clone 7559623
5	similar to gb:u72467 UG KAPPA CHAIN PRECURSOR V-II REGION

۱۰۰

High quality sequence stops: 1
Source: IMAGE Consortium, LNL
--This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality.
Location/Qualifiers
1
353

BASE COUNT ORIGIN	53 a	67 c	62 g	63 t	12 others
----------------------	------	------	------	------	-----------

Query Match	36.68	Score 144.8	DB 10	Length 257
Best Local Similarity	71.48	Pred. No. 8,4e-36		
Matches 182, Conservative	0	Mismatches 73	Indels 0	Gaps 0

[illegible]

Search completed: May 11, 1999, 11:44:10
Job time: 497 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:37:53 ; Search time 88.51 Seconds
(without alignments)
841.712 Million cell updates/sec

Title: US-08-700-737-11

Sequence: 1 ATGAAGTTGCCTGTTAGGCT.....GGACCAAGCTGGAATAAAA 396

Scoring table:

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	ID	Description	
No.	Score		DB			
1	396	100.0	396	1	V20077	DNA encoding murin
2	396	100.0	535	1	V20086	Consensus DNA sequ
3	359.2	90.7	413	1	V20075	DNA encoding the I
4	296.8	74.9	717	1	T62934	Murine anti-porcine
5	296.8	74.9	5300	1	T62938	3F4 human IgG4 exp
6	293.6	74.1	394	1	062763	Murine anti-porcine
7	293.6	74.1	394	1	062788	Murine KC-4 immuno
8	292	73.7	394	1	087531	Murine KC-4 immuno
9	288.8	72.9	394	1	062803	Humanised murine K
10	288.8	72.9	394	1	087533	Humanised murine K
11	287.2	72.5	394	1	062749	Humanised anti-KC-4
12	287.2	72.5	394	1	062774	Murine BRE-3 immuno
13	286	72.2	384	1	V56383	Murine BRE-3 immuno
14	286	72.2	384	1	V56383	Murine ICR-8.1 V-K
15	285.6	72.1	537	1	014651	Murine antibody IC
16	284	71.7	437	1	036529	R6-5-D6 anti-ICAM
17	284	71.7	437	1	036536	Chimeric Mab 11g
18	284	71.7	437	1	T31332	BR55-2 light chain
19	284	71.7	444	1	T98835	Anti-idiotypic mono
20	282.4	71.3	434	1	Q36534	Coding sequence fo
21	282.4	71.3	394	1	Q62790	BR55-2 murine IgG3
22	282.4	71.3	717	1	T88870	Humanised murine B
23	282.4	71.3	396	1	V37265	l chain subunit oB
24	282.4	71.3	717	1	V6736	CDNA encoding a va
25	279.2	70.5	8897	1	V18692	Anti-human Fas mon
26	277.6	70.1	537	1	014601	Plasmid pTMD-CIVK
27	276	69.7	422	1	V22075	Encodes murine anti
28	274.4	69.3	420	1	V60831	DNA encoding the l
29	272.8	68.9	432	1	008606	Variable light chain
30	272.8	68.9	432	1	T43439	Co-1 light chain v
31	269.4	68.0	459	1	011392	Mab Co-1 light cha
32	269.2	68.0	330	1	Q43746	Encodes murine mon
33	266.8	67.4	861	1	081500	Sequence encoding
34	266.8	67.4	861	1	T45347	sFv anti-rev sequen
35	266.4	67.3	388	1	V66674	Single chain sFv a
36	255	64.4	782	1	086755	Anti-Fas MAb CH11
37	252	63.6	413	1	Q20071	Anti-dansyl single
38	251.2	63.4	336	1	Q97505	MRK16-F chain. Chl
39	250.4	63.2	876	1	V10390	Light chain variabl
40	250.4	63.2	8897	1	V18693	Monoclonal anti bod
41	249.6	63.0	336	1	T36587	Plasmid pDi6h71.11
42	248.8	62.8	747	1	Q21098	DNA encoding murin
43	248.8	62.8	733	1	V10375	pScFvN01 encoding
						Anti-CD40 monoclon

QY 241 TCTGGGTCGCAGACAGTTCAGTGCAGTTCAGGACAGATTTCACACTCAGATC 300
 DB 241 TCTGGGTCGCAGACAGTTCAGTGCAGTTCAGGACAGATTTCACACTCAGATC 300
 QY 301 AGCACATAAAGCCTGAGAGCTTGGAAATGATATCTGCTTACAGGATACATCAGCCG 360
 DB 301 AGCACATAAAGCCTGAGAGCTTGGAAATGATATCTGCTTACAGGATACATCAGCCG 360
 QY 361 TACAGCTTCGAGGGGGGACCAAGCTGGAATATAA 396
 DB 361 TACAGCTTCGAGGGGGGACCAAGCTGGAATATAA 396

RESULT 2

V20086 standard; DNA; 535 BP.
 AC V20086:
 DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.
 FT Key Location/Qualifiers
 FT CDS 16..435
 FT sig_peptide /tag= a
 FT 16..75 /note= "no stop codon given"
 FT mat_peptide /tag= b
 FT 76..435
 FT /tag= c
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J.
 PI WPI: 98-159172/14.
 DR P-PsDB: W53817.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3: 145pp: English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 CC Sequence 535 BP; 126 A; 128 C; 132 G; 149 T;

Query Match

100.0%; Score 396; DB 1; Length 535;

Best Local Similarity 100.0%; Pred. No. 4, 2e-116;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTTGCCCTGTAGGCTGTGGTCTCTGTGCTGAGATTCCTGTTCCGAGGT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 16 ATGAGTTGCCCTGTAGGCTGTGGTCTCTGTGCTGAGATTCCTGTTCCGAGGT 75
 QY 61 GATGTGTGGTACCAAACTCCACTCCCTGCTGTCAGATTGGAGATCAAGTTCT 120
 DB 76 GATGTGTGGTACCAAACTCCACTCCCTGCTGTCAGATTGGAGATCAAGTTCT 135
 QY 121 ATCTCTGAGGTCTAGTCAGAGTCTTCCAAAGATTATGGACACCTATTGTCTGG 180
 DB 136 ATCTCTGAGGTCTAGTCAGAGTCTTCCAAAGATTATGGACACCTATTGTCTGG 195
 QY 181 TACCTGCACACAGCTGGCCAGTCTCCACAGCTCCCTCATCTATGGATTTCACAGATT 240
 DB 196 TACCTGCACACAGCTGGCCAGTCTCCACAGCTCCCTCATCTATGGATTTCACAGATT 255
 QY 241 TCTGGGTCGCAGACAGTTCAGTGCAGTTCAGGACAGATTTCACACTCAGATC 300
 DB 256 TCTGGGTCGCAGACAGTTCAGTGCAGTTCAGGACAGATTTCACACTCAGATC 315
 QY 301 AGCACATAAAGCCTGAGAGCTTGGAAATGATATCTGCTTACAGGATACATCAGCCG 360
 DB 316 AGCACATAAAGCCTGAGAGCTTGGAAATGATATCTGCTTACAGGATACATCAGCCG 375
 QY 361 TACAGCTTCGAGGGGGGACCAAGCTGGAATATAA 396
 DB 376 TACAGCTTCGAGGGGGGACCAAGCTGGAATATAA 411

RESULT 3

V20075 standard; DNA; 413 BP.
 AC V20075:
 DT 14-JUL-1998 (first entry)
 DE DNA encoding the light chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Synthetic.
 OS Mus sp.
 FT Key Location/Qualifiers
 FT CDS 1..413
 FT sig_peptide /tag= a
 FT 1..60 /transl_except= (pos: 412..413, aa: Pro)
 FT mat_peptide /tag= b
 FT 61..413 /note= "no stop codon given"
 FT /tag= c
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J.
 PI WPI: 98-159172/14.
 DR P-PsDB: W53812.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Clam 17; Fig 12: 145pp: English.
 CC The present sequence encodes the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can

QY 381 CAAAGCTGGAATATAA 396
 Db 369 CAAAGCTGGAATATAA 384

RESULT 15

Q14651
 ID Q14651 standard; cDNA; 537 BP.
 AC Q14651;
 DT 14-FEB-1992 (first entry)
 DE R6-5-D6 anti-ICAM-1 light chain.
 KW Intercellular adhesion molecule-1; antibody; chimeric; ds.
 OS Mus musculus.
 FH Key
 FT signal_peptide Location/Qualifiers
 FT 19..75
 FT /*tag- a
 FT 19..537
 FT /tag- b
 FT cds
 PN WO9116928-A.
 PD 14-NOV-1991.
 PE 29-APR-1991; U02946.
 PR 27-APR-1990; GB-009548.
 PA (CELL-) CELLTECH LTD.
 PI (BOEH) BOEHRINGER INGELHEIM PHA.
 PI Adair JR, Robinson MK, Bright SM, Rothlein RA;
 DR WPI; 91-353534/48.
 DR P-PADB; R15199.
 PT New humanised chimeric anti-ICAM-1 antibodies - useful in
 PT treating inflammation e.g. psoriasis and ulcerative colitis to
 PT suppress metastasis of haematopoietic tumour cell and in
 PT diagnosis.
 PS Claim 10; Fig 1; 85pp; English.
 PS The sequence comprises the 5' untranslated region, signal sequence,
 CC variable region and part of the constant region for the R6-5-6D
 CC murine MAb light chain. The hybridoma cell line R6-5-D6 producing
 CC the anti ICAM-1 Ab was provided by Boehringer Ingelheim
 CC Pharmaceuticals Inc. The cells were grown and mRNA isolated and
 CC used to prepare cDNA for a library in pSP64 vector DNA. The
 CC library was grown in E. coli HB101 and colonies screened using a
 CC probe complementary to a sequence in the mouse kappa constant
 CC region or with a 980 bp BamHI-EcoRI restriction fragment of a
 CC previously isolated mouse IgG2a constant region clone. Six
 CC positive clones were isolated and rescreened. Positive clones from
 CC the second round of screening were grown and the DNA inserts
 CC sequenced. The DNA was used to construct humanised Abs having
 CC chimeric variable regions, esp. with IgG human constant region
 CC domains. The Abs can be used to treat inflammation, to suppress
 CC metastasis of haematopoietic tumour cells and growth of ICAM-1
 CC expressing tumour cells, to treat viral infection, to suppress
 CC extravascular migration of virally infected leucocytes and to treat
 CC asthma.
 CC See also Q14652 and Q14830.
 SQ Sequence 537 BP; 135 A; 134 C; 128 G; 139 T;

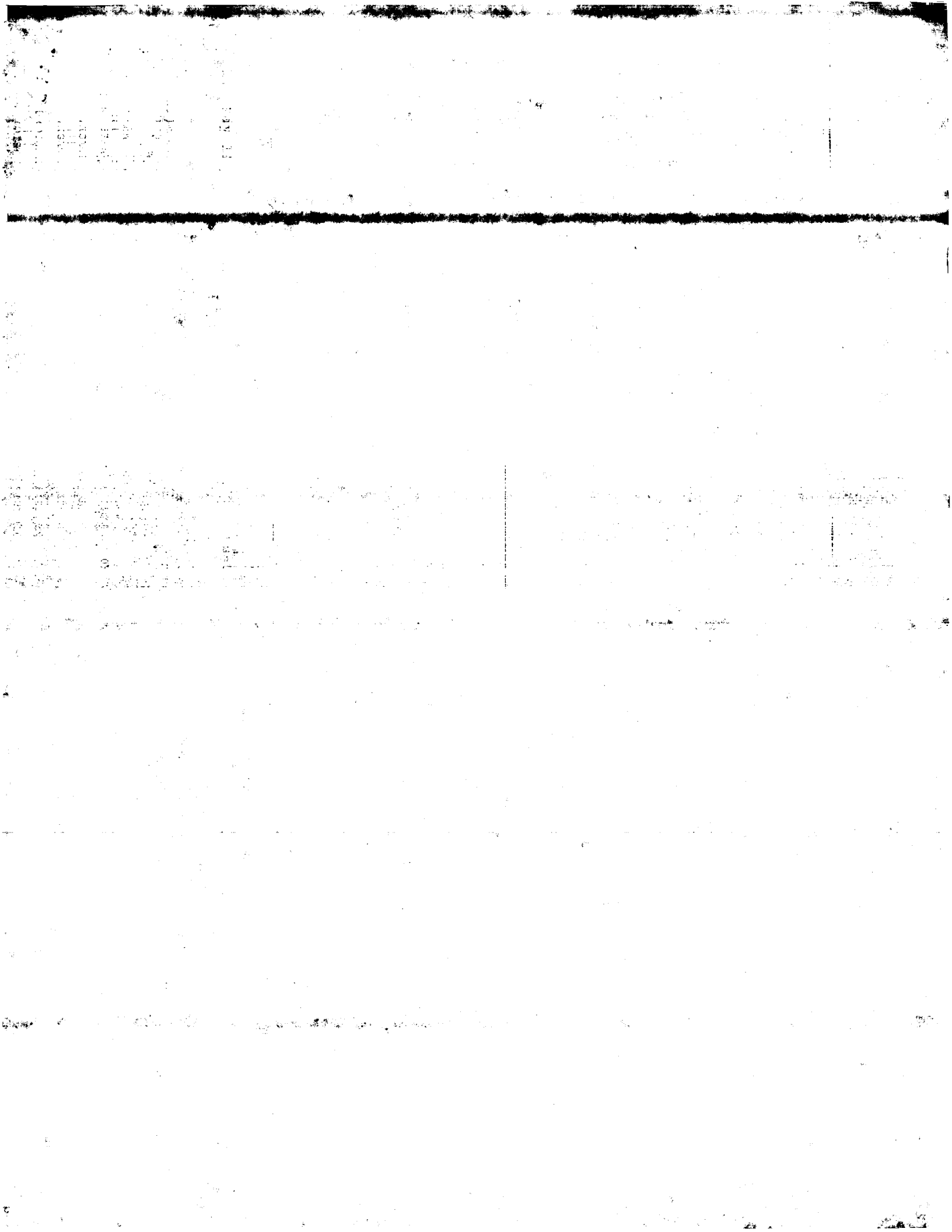
Query Match

Best local Similarity 72.1%; Score 285.6; DB 1; Length 537;
 Matches 334; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTTCTGATTCCTGTTCCGGAGGT 60
 Db 19 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTTCTGATTCCTGATTCAGCAGT 75
 QY 61 GATGTTGTGTGACTCAAACTCCATCTCCCTGCTGCTTGTGAGATCAAGTTCT 120
 Db 76 GATGTTGTGTGACTCAAACTCCATCTCCCTGCTGCTTGTGAGATCAAGCTCC 135
 QY 121 ATCTCTTGCAAGTCTAGTCAAGTCTTGAAGAAGTATGGAACACCTATTTGCTTG 180
 Db 136 ATCTCTTGCAAGTCTAGTCAAGTCTTGAAGAAGTATGGAACACCTATTTGCTTG 195
 QY 181 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAAAGATT 240

Db 196 TACCTGCACAAAGCTGGCCAGTCTCCACAGCTCCTCATCTATGGGATTTCCAAAGATT 255
 QY 241 TCTGGGGTGCACAGACAGGTTCAAGTGTGAGGACAGATTTCACTACAGATC 300
 Db 256 TCTGGGGTGCACAGACAGGTTCAAGTGTGAGGACAGATTTCACTACAGATC 315
 QY 301 AGCACAATAAAGCTGAGGACTTGGGAATGTATTACTGTTACAAAGTACATCAGCG 360
 Db 316 AGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTCTGCTCAAAAGTACATGTTCT 375
 QY 361 TACAGCTTGGAGGGGGGACCAAGCTGGAATATAA 396
 Db 376 CTCACGTTGGAGGGGGGACCAAGCTGGAATATAA 411

Search completed: May 11, 1999, 12:03:26
 Job time: 1533 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:18:27 ; Search time 30.48 Seconds
(without alignments)
162.230 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPTFGGQTKLEIK 132

Scoring table: BLOSUM62

Searched: 116738 seqs, 37460341 residues

Database: PIR-58.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	620	89.2	132	2	B25912	Ig kappa chain pre
2	576	82.9	113	2	H30560	Ig kappa chain V r
3	574	82.6	113	2	E30560	Ig kappa chain V r
4	563	81.0	112	2	S37203	Ig kappa chain V r
5	560.5	80.6	131	2	B39276	Ig light chain pre
6	553.5	79.6	131	2	B34904	Ig kappa chain pre
7	549.5	79.1	131	2	C34904	Ig kappa chain pre
8	548.5	78.9	114	2	PL0202	anti-DNA autoantib
9	546.5	78.6	131	2	B32513	Ig kappa chain pre
10	545.5	78.5	131	2	B30577	Ig kappa chain pre
11	540.5	77.8	132	3	D34904	Ig kappa chain pre
12	540.5	77.6	131	2	PH0106	anti-digoxin trans
13	539	77.3	131	2	D29380	Ig kappa chain pre
14	537.5	77.3	131	2	G34903	Ig kappa chain pre
15	537.5	77.3	131	2	PS0074	Ig kappa chain V r
16	536.5	77.2	131	2	S09259	Ig kappa chain pre
17	529.5	76.2	131	2	S52449	Ig kappa chain pre
18	523.5	75.3	131	2	PI0178	Ig kappa chain pre
19	521	75.0	130	2	C29380	Ig kappa chain pre
20	502	72.2	133	2	S23230	Ig kappa chain pre
21	497.5	71.6	119	2	A49032	Ig kappa chain pre
22	496	71.4	142	2	S22902	Ig kappa chain V r
23	493.5	71.0	118	2	S24503	Ig kappa chain V r
24	493	70.9	133	2	S42611	HDMVX protein prec
25	492.5	70.9	118	2	S24536	Ig kappa chain V r
26	491	70.6	133	1	K2HURP	Ig kappa chain pre
27	490.5	70.6	118	2	S24533	Ig kappa chain V r
28	489	70.4	112	2	E27887	Ig kappa chain V r
29	488.5	70.3	118	2	S24500	Ig kappa chain V r
30	488	70.2	118	2	PI0359	Ig kappa chain V r
31	488	70.2	112	2	A31807	Ig kappa chain V r
32	487.5	70.1	118	2	S24529	Ig kappa chain V r
33	487.5	70.1	118	2	S24535	Ig kappa chain V r
34	486	69.9	112	2	A49715	Ig kappa chain V r
35	486	69.9	219	2	S16112	Ig kappa chain V r
36	484	69.6	110	2	S26335	Ig kappa chain V r
37	484	69.6	121	2	S67944	Ig kappa chain pre
38	483	69.5	112	2	S32189	Ig kappa chain V r
39	483	69.5	113	2	PL0203	anti-DNA autoantib

40 481.5 69.3 140 2 S22658 Ig kappa chain pre
41 481.5 69.3 118 2 S24532 Ig kappa chain V r
42 481 69.2 112 2 B31485 Ig kappa chain V r
43 481 69.2 219 2 PC4203 Ig kappa chain (mo
44 480.5 69.1 118 2 S24530 Ig kappa chain V r
45 480 69.1 112 2 D27887 Ig kappa chain V r

ALIGNMENTS

RESULT 1
B25912
Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Mar-1998
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912
A:Molecule type: mRNA
A:Residues: 1-132 <BOR>
A:Cross-references: GB:M15874; NID:g196839; PID:g196840
A:Note: the authors translated the codon CTC for residue 120 as Ser
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:1-19/Domain: signal sequence (fragment) #status predicted <Sig>
F:20-132/Product: Ig kappa chain V region W3129 #status predicted <Var>

Query Match 89.2%; Score 620; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 5.1e-51;
Matches 118; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 3 LPVRLVLLFWIPVSGGVVVTQTPLSPVSGDVSICRSSQSLAKSYGNTYLSWYL 62
Db 2 LPVRLVLLFWIPASRDVVVTQTPLSPVSGDVSICRSSQSLATSHGITYLSWYL 61

Oy 63 HKPQSPQLLYGTSNRPSPGDPDRFSGSGSTDTTKISTIKPDLGMYVLOSTHQPRT 122
Db 62 HKPQSPQLLYGTSNRPSPGDPDRFSGSGSTDTTKIKPDLGMYVLOSTHQPRT 121

Oy 123 FGAGTKLEIK 132
Db 122 FGAGTKLEIK 131

RESULT 2
H30560
Ig kappa chain V region (36.1.2D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 20-Mar-1998
C:Accession: H30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
A:Reference number: A30560; MUID:89110062
A:Accession: H30560
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAT>

A:Cross-references: GB:M24275; NID:g197085; PID:g197086
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin

Query Match 82.9%; Score 576; DB 2; Length 113;
Best Local Similarity 97.3%; Pred. No. 5.3e-47;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

A:Reference number: A30560; MUID:89110062
A:Accession: E30560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAT>
A:Note: the authors translated the codon GTA for residue 30 as His
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Oy 21 DVVATQTPLSEVSFGDDVYSISCSHSSQSLAKSYGNITLSWYLHKPGQSPLLIGISNRF 80
Db 1 DVVATQTPLSEVSFGDDVYSISCSHSSQSLAKSDGNTLSWYLHKPGQSPLLIGISNRF 60

OY 81 SGVDFRFGSGGSDFTLKISTINPEDLGMYCYCQGTHTOPRYTEGGGKLEIK 132
| | | | | : | | | | |
DB 61 SGVPDRFSSGSGSDFTLKISTINPEDLGMYCYCQGTHTQPWFTEGGGKLEIK 112

RESULT 4
S37203
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S37203
R:Flischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
Submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of MW-specific monoclonal antibodies
Reference number: S37200

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <RTS>
A;Cross-references: EMBL:X74588; NID:q20297; PID:c86056; PID:g1333960
C;Superfamily: Immunoglobulin V region; Immunoglobulin homology

Query Match	81.0%	Score 563	DB 2	Length 112
Best Local Similarity	94.6%	Pred. No. 8.5e-46		
Matches 106; Conservative	3	Mismatches 3	Indels 0	Gaps 0

Oy 21 DVVVTQTPLSLPVSFSGDQVSISSCSQSLSAKSYGNTYLSWYLHKPGQSPQLLIYGISNRF 800
 |||||
 :
Db 1 DVVVTQTPLSLPVSFSGDQVSISSCSQSLSANSGYNTHLSWLHLKPGQSPQLLIYGISNRF 600
 |||||

QY 81 SGVPDRFSGSGGSDFTLKISTKPEDLGMYCYCQGTHTQPPTFGGGTKEIK 132
| | | | | | | | | | | | | | | | : | | | :
DB 61 SGVPDRFSGSGGSDFTLKISTKSSED LGMYCYCQGTHTQPFTEGAGTKLEK 112

Query Match	80.6%	Score	560.5	DB 2	Length	131			
Best Local Similarity	80.3%	Pred. No.	1.7e-45						
Matches	106	Conservative	10	Mismatches	15	Indels	1	Gaps	1

QY 1 MKLPRLVLLFWIPVSGGVVVTQTPLSLPVSGDQVQISCRSSQSLAKSGNTLYLW 60
| | | | | : | | | | | | | | | | | | | | | : | | | | |
| | | | | ~ | | | | | | | | | | | | | | | : | | | | |
Db 1 MKLPRLV-LFWIPVSSVDVINTQTPLSLPVSLGDAQASISCRSSQSIIVHNGNTLYLW 59

```

QY 61 YLHRGQSPDLLIYGISNRFSGVDPDRRSGSGSGTDFTLKISTIKEDLGMYCYLGTHQP 120
    || |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 YLQKPGQSPKLLIKYKSNRFSGVDPDRSGSGSGTDFTLKISRVEADLGVYCYFCQGSHP 119

```

```

OY      121 YTFGGGTTKLEIK 132
        1111 11111111
Db      120 YTFGSGTKLEIK 131

```

RESULT 6
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C:Accession: B34904; H34903
R:Bedzlyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J Biol Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-
A:Reference number: A34903; MUID:90094387

A: Status: preliminary; not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-131 <BDD>
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin

Query Match	79.6%	Score 553.5;	DB 2,	Length 131;
Best Local Similarity	80.3%	Pred. No. 7.7e-45;		
Matches 106; Conservative	9;	Mismatches 16;	Indels 1;	Gaps 1.

```

1 MKLEPYRLV-LMFWIPASSSDVVMTOIPLSPLVSLGDAQSISCRSSQSLVHSNGNTYLLHW 59

```

```

Db      60 YLQKPGQSPALLIKVSNRFGVPPDRFGSGSGSTFTLKISRVEAEDLGVYFCSQSSTHP 119

```

```
QY      121 YTFGGGKTLEIK 132
      : |||||
Db      120 WTFGGGKTLEIK 131
```

RESULT 7
C34904

Ig kappa chain precursor V region (3-24) - mouse
C:Species: Mus musculus (house mouse)
C:/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 13-Mar-1997
C:/Accession: C34904; 131485
R:/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:/Title: Active site structure and antigen binding properties of idiotypically cross-reactive reference number: A34903; M0ID:90094387
A:/Accession: C34904
A:/Status: preliminary; not compared with conceptual translation
A:/Molecule type: mRNA
A:/Residues: 1-131 <BED>
R:/Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A:/Title: Comparison of variable region primary structures within an anti-fluorescein idiotype reference number: A31485; M0ID:89109167
A:/Accession: 131485
A:/Status: preliminary
A:/Molecule type: protein
A:/Residues: 20-52 <BED>
C:/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:/Keywords: heterotetramer; Immunoglobulin

Query Match 79.1%; Score 549.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 1.8e-44;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
Db 1 MKLPVRLVLLFWIPVSGDVVVTQTPSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
1 MKLPVRLV-LFWIPVSSSDVVTQTPSLPVSFGDQVSISSCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 120
60 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 119
Db 121 YTFGGGTKEIK 132
120 WTFGGGTKEIK 131

RESULT 8
PLOT202
anti-DNA autoantibody BV16-13, kappa chain V region - mouse (fragment)
C:/Species: Mus musculus (house mouse)
C:/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
C:/Accession: PLOT202
R:/Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:/Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N/A; Reference number: PLOT198
A:/Accession: PLOT202
A:/Molecule type: mRNA
A:/Residues: 1-114 <SMI>
C:/Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:/24-39/Region: complementarity-determining 1
F:/55-61/Region: complementarity-determining 2
F:/94-103/Region: complementarity-determining 3
F:/102-114/Region: JH region

Query Match 78.9%; Score 548.5; DB 2; Length 114;
Best Local Similarity 94.7%; Pred. No. 1.9e-44;
Matches 107; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
QY 21 DVVYVTPPLSPVSPVSGDQVSISSCRSSQSLAKSYGNTYLSWYLRKPGSPQLLYGSISSNR 80
1 DVVYVTPPLSPVSPVSGDQVSISSCRSSQSLAKSYGNTYLSWYLRKPGSPQLLYGSISSNR 60
Db 1 DVVYVTPPLSPVSPVSGDQVSISSCRSSQSLAKSYGNTYLSWYLRKPGSPQLLYGSISSNR 60
QY 81 SGVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP-YTFGGGTKEIK 132
61 SGVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP-YTFGGGTKEIK 113

RESULT 9
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C:/Species: Mus musculus (house mouse)
C:/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
C:/Accession: B32513
R:/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
J. Clin. Invest. 82, 852-860, 1988
A:/Title: Immunoglobulin kappa light chain variable region gene complex organization
A:/Reference number: A94689; M0ID:88331384
A:/Accession: B32513
A:/Molecule type: DNA
A:/Residues: 1-131 <KOF>
A:/Cross-references: GB:M20828; NID:916937; PID:916938
C:/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:/Keywords: heterotetramer; Immunoglobulin

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 3.4e-44;
Matches 105; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
1 MKLPVRLV-LFWIPVSSSDVVTQTPSLPVSFGDQVSISSCRSSQSLVHSGNTYLSW 59
Db 61 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 120
60 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 119
QY 121 YTFGGGTKEIK 132
120 YTFGGGTKEIK 131

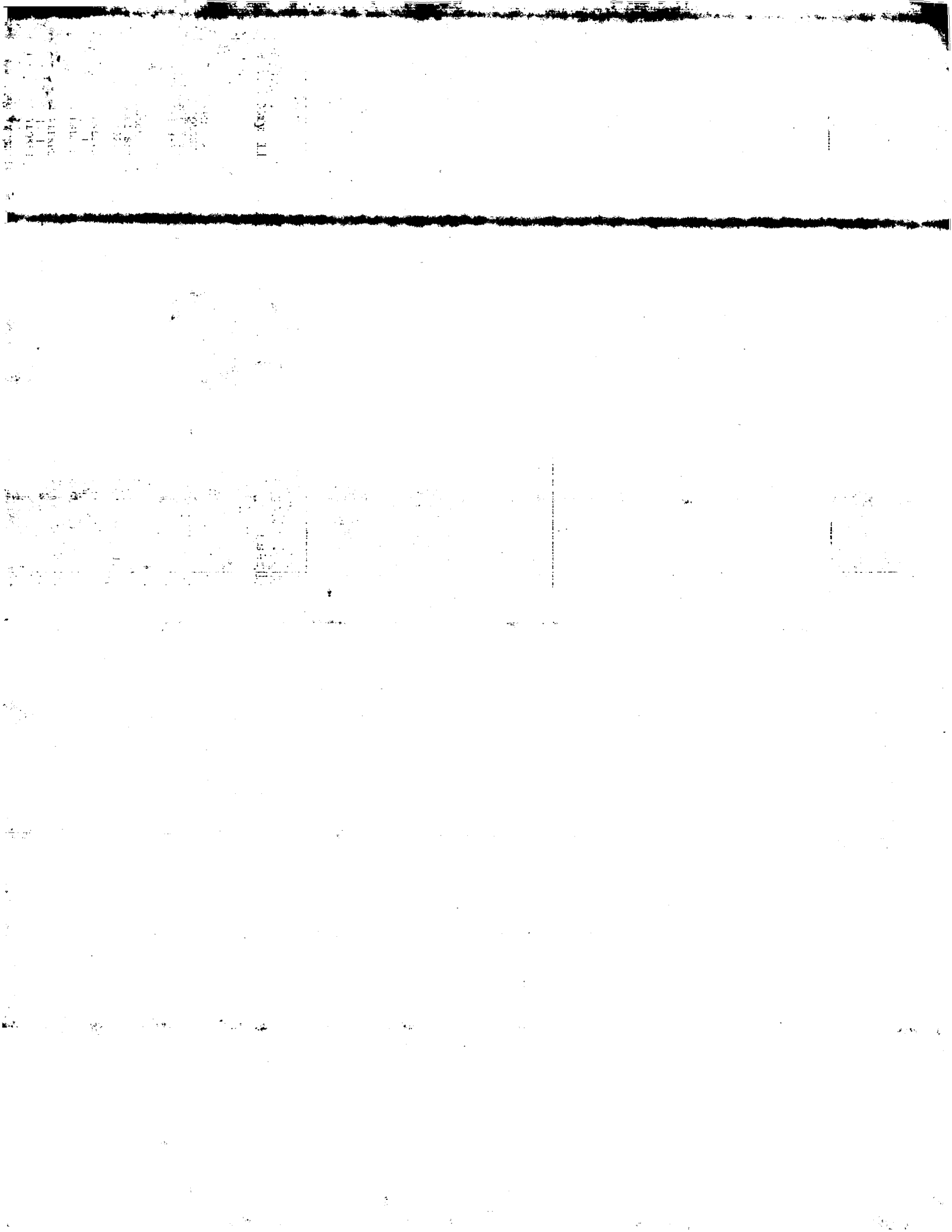
RESULT 10
B30577
Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C:/Species: Mus musculus (house mouse)
C:/Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C:/Accession: B30577
R:/Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A:/Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A:/Reference number: A30577; M0ID:85159423
A:/Accession: B30577
A:/Status: preliminary; not compared with conceptual translation
A:/Molecule type: mRNA
A:/Residues: 1-131 <KOF>
C:/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:/Keywords: heterotetramer; Immunoglobulin

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 3.4e-44;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
1 MKLPVRLV-LFWIPVSSSDVVTQTPSLPVSFGDQVSISSCRSSQSLVHSGNTYLSW 59
Db 61 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 120
60 YLHKPGSPQLLYGSISSCRSSGSDVDFRFGSGSDFTLKSTIKPEDLGMYCLOGTROP 119
QY 121 YTFGGGTKEIK 132
120 YTFGGGTKEIK 131
RESULT 11
B34904

A:Accession: P50074
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-111 <LEV>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 77.3%; Score 537.5; DB 2; Length 111;
 Best Local Similarity 92.9%; Pred. No. 2e-43;
 Matches 104; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
 QY 21 DVVVTQTPLSLPVSGDQVSISCRSSQSLAKSYGNTYLSWYHLKPGQSPOLLITYGISNRF 80
 Db 1 DVVVTQTPLSLPVSGDQVSISCRSSQSLANSSTYGNLYLSWYHLKPGQSPOLLITYGISNRF 60
 QY 81 SGVPRFSGSGSGTDFTLKISTIKPEDLGWYCIQGTHTQPTFGGKLEIK 132
 Db 61 SGVPRFSGSGSGTDFTLKISTIKPEDLGWYCIQGTHTQ-LTFGAGKLEIK 111

Search completed: May 11, 1999, 12:23:24
 Job time: 297 sec



QX. 18 SGGDVVVTQTPLSLPSVSEFGDQVSI SCRSSQSLAKSYGNTYLSWY LHKPGOSPOLLITYGIS

OC EUTHERIA; PRIMATES.

-Query Match:	56.98;	Score 395.5;	DB 1;	Length 112;
Best Local Similarity	65.28;	Pred. No. 8.5e-33;		

RESULT	11
KY2F_MOUSE	
ID	KY2F_MOUSE
AC	P01630;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN V-II REGION (7534.1).
OS	MUS MUSCULUS (MOUSE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE.
RX	MEDLINE. 83256427.
RA	CHANG J.-Y., HERBST H., ABERGOLD R., BRAUN D.G.;
RL	BIOCHEM. J. 211:173-180(1983).

OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041854.
 RA MARSH P., MILLS F., GOULD H.;
 RL NUCLEIC ACIDS RES. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA MARSH P.;
 RL SUBMITTED (OCT-1986) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X02990; G37910; -
 DR PIR: A01905; KAHU17.
 DR HSSP: P01607; 21MN.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 134 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 55.5%; Score 385.5; DB 1; Length 134;
 Best Local Similarity 57.1%; Pred. No. 1e-31;
 Matches 76; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 1 MKLPRLVLLFWIPVSGGVVYTOPPLSPVSGDQVSSICRSSQSILAKSYGNTYLS 59
 1 MVLQTVFISLLWISGAYGDIWMTQSPDSLAVSGERATINCKSSQSIILYSDMKNYLA 60
 DB 60 WYLRPGSPOLLIVGISNRFSGVDPDRFSGSGGTFTLKISTIKPEDLGMYTCLOGTHQ 119
 61 WYQKRGSPRLIINDASSRANGIPDRFSGSGGTFTLISRLEPEDFAVYYCQYSTSP 120
 DB 120 PYFGGSTRLEIK 132
 121 PWTFGGSTRLEIK 133

RESULT 15
 KV3K HUMAN STANDARD; PRT: 128 AA.
 ID P06311;
 AC 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
 OS HOMO SAPIENS (HUMAN)
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA KLOBECK H.G., MEINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
 DR EMBL: Z00021; G33179; -
 DR PIR: A01899; K3HU41.
 DR HSSP: P01607; 3HEM.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 118 128 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match 54.7%; Score 380.5; DB 1; Length 128;
 Best Local Similarity 55.3%; Pred. No. 3.1e-31;
 Matches 73; Conservative 26; Mismatches 28; Indels 5; Gaps 1;

QY 1 MKLPRLVLLFWIPVSGGVVYTOPPLSPVSGDQVSSICRSSQSILAKSYGNTYLS 60
 1 MTPAQLEFLMLWLPDTGELVLTQSPGTLSLSPGESATLSCRASQSVSN-----LAW 55
 DB 61 WYLRPGSPOLLIVGISNRFSGVDPDRFSGSGGTFTLKISTIKPEDLGMYTCLOGTHQ 120
 56 WYQKRGSPRLIINDASSRANGIPDRFSGSGGTFTLISRLEPEDFAVYYCQYSTSP 115
 QY 121 YTFGGSTRLEIK 132
 116 YTFGGSTRLEIK 127

Search completed: May 11, 1999, 12:20:08
 Job time: 305 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:16:48 ; Search time 38.54 Seconds

(without alignments)
188.955 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MLLPVRLVLLFWIPVSGG.....CLOGTHQPYTGGGTRLEIK 132

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

SPREMBL-8:*
1: sp_fungi:*
2: sp_human:*
3: sp_invertebrate:*
4: sp_mmc:*
5: sp_mmc:*
6: sp_organelle:*
7: sp_phage:*
8: sp_plant:*
9: sp_bacteria:*
10: sp_rodent:*
11: sp_virus:*
12: sp_vertebrate:*
13: sp_unclassified:*
14: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	371	53.4	100	2	Q15535	Q15535 homo sapien
2	315	45.3	130	10	P80913	P80913 mus musculu
3	148	21.3	513	10	P97797	P97797 mus musculu
4	146	20.7	509	10	O08907	O08907 mus musculu
5	144	20.7	509	10	O35924	O35924 mus musculu
6	137	19.7	509	10	O88555	O88555 mus musculu
7	137	19.7	291	10	O88556	O88556 mus musculu
8	134.5	19.4	50	2	Q15533	Q15533 homo sapien
9	132.5	19.1	132	5	Q11175	Q11175 mus musculu
10	129.5	18.6	145	2	Q16237	Q16237 homo sapien
11	129.5	18.6	135	5	Q31174	Q31174 mus musculu
12	126.5	18.2	133	10	O61243	O61243 mus musculu
13	125.5	18.1	210	4	P79336	P79336 felis silve
14	119.5	17.2	509	10	P97710	P97710 rattus norv
15	115.5	16.6	418	10	O70426	O70426 rattus norv
16	112	16.1	134	5	Q31180	Q31180 mus musculu
17	109.5	15.8	135	2	O99602	O99602 homo sapien
18	109	15.7	133	5	Q31178	Q31178 mus musculu
19	105.5	15.2	132	5	Q31177	Q31177 mus musculu
20	104.5	15.0	401	4	O08835	O08835 ceropithe
21	104	15.0	506	4	O46632	O46632 bos taurus
22	104	15.0	137	5	Q31181	Q31181 mus musculu
23	102	14.7	372	2	Q15267	Q15267 homo sapien
24	102	14.7	364	2	Q15268	Q15268 homo sapien
25	100.5	14.5	118	5	Q31176	Q31176 mus musculu
26	99.5	14.3	228	10	O70153	O70153 rattus norv
27	98.5	14.2	254	12	O90557	O90557 ginglymosto
28	97.5	14.0	503	2	P78324	P78324 homo sapien
29	97.5	14.0	117	5	Q31278	Q31278 rattus norv

30	97	14.0	198	2	Q13970	Q13970 homo sapien
31	97	14.0	506	4	O46631	O46631 bos taurus
32	97	14.0	157	12	O90539	O90539 ginglymosto
33	96	13.8	158	12	O90531	O90531 ginglymosto
34	94	13.5	252	12	O90568	O90568 ginglymosto
35	92.5	13.3	398	2	O00241	O00241 homo sapien
36	92.5	13.3	119	2	O99599	O99599 homo sapien
37	92.5	13.3	121	2	O99600	O99600 homo sapien
38	91	13.1	233	5	Q31127	Q31127 mus musculu
39	91	13.1	133	12	O90553	O90553 ginglymosto
40	90.5	13.0	113	12	O90552	O90552 ginglymosto
41	90.5	13.0	145	12	O90555	O90555 ginglymosto
42	90.5	13.0	250	12	O90569	O90569 ginglymosto
43	89.5	12.9	139	12	O90524	O90524 ginglymosto
44	89	12.8	139	12	O90533	O90533 ginglymosto
45	88.5	12.7	1021	2	Q15856	Q15856 homo sapien

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	Q15535	PRELIMINARY; PRT; 100 AA.
AC	Q15535;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	
DE	V KAPPA (FRAGMENT).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;	
OC	CATARRHINI; HOMINIDAE; HOMO.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	KATO S., TACHIBANA K., TAKAYAMA N., KATAOKA H., YOSHIDA M.C.,	
RA	TAKANO T.;	
RL	SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.	
DR	EMBL; D90161; G1262585; -	
DR	PFAM; PF00047; 1g; 1.	
FT	NON_TER 1 100	
FT	NON_TER 1 100	
SQ	SEQUENCE 100 AA; 10871 MW; 06A1440D CRC32;	
Query Match	53.4%; Score 371; DB 2; Length 100;	
Best Local Similarity	72.0%; Pred. No. 3.6e-28;	
Matches	72; Conservative 10; Mismatches 18; Indels 0; Gaps 0;	
QY	21 DVTVTQPLSLPVSPFGDVSISGRSSQSLAKSYGNTLSWYLRKPGSPQQLLYGISNRF 80	
DB	1 DVTWQTPPLSLVTPGPGPASISCKSLSLHSDGKTLXYLAKPGSPQQLLYEVSRRF 60	
QY	81 SGVDRFSGSGSGTDFLTKISTIKPEDLGWYICLOGTHOP 120	
DB	61 SGVDRFSGSGSGTDFLTKISRVAEADVGYCYMGQIHLP 100	
RESULT	2	
ID	P80913	PRELIMINARY; PRT; 130 AA.
AC	P80913;	
DT	01-NOV-1998 (TREMBLREL. 08, CREATED)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)	
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)	
DE	IG KAPPA CHAIN V REGION PRECURSOR.	
OS	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;	
OC	SCIUROGNATHI; MURIDAE; MORINAE; MUS.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	UNION K.;	
RL	SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.	
DR	EMBL; X79906; E269393; ALT_TERM.	


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Db 15 LILCLILSLASCFCTGATGTEVKYTOPEKSYSAAGDSTILNCTVTSILPVG----PIRW- 70
QY 63 HKPGSGPOLLITYGISN----RESGVPDRSSGSGSDTFLKSTIKPEDLGMYCL--Q 115
      |||:|||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 70 RGVGGS-RLIYSFTGEHPRVRYNSD--TKRNNMADFIRISNVPEDAGTYCYVKFOR 126
      |||:|||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 116 GTHQPYT---FGGCKLEI 131
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 127 GSSEPDTEIOSGGTEVYV 145
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 5
ID 035924 PRELIMINARY; PRT; 509 AA.
AC 035924;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1, PRECURSOR...
DE (P84).
GN PTPNS1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCUROGNATHI; MORIDA; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9801243.
RX COMU S., WENG W., OLINSKY S., ISHWAD P., MI Z., HEMPEL J., WATKINS S.,
RA LAGENAUR C.F., NARAYANAN V.;
RT "The murine p84 neutral adhesion molecule is SHPS-1, a member of the
RL phosphatase-binding protein family."
DR J. NEUROSCI. 17:8702-8710(1997).
DR EMBL; U89694; G2580535; -.
DR MGD; MGI:108563; PTPNS1.
DR PFM; PF00047; 1g; 3.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL. 1 31 POTENTIAL.
FT CHAIN 32 509 P84.
SQ SEQUENCE 509 AA; 56056 MW; 3A781050 CRC32;

Query Match 20.7%; Score 144; DB 10; Length 509;
Best Local Similarity 33.1%; Pred. No. 4.3e-06;
Matches 46; Conservative 24; Mismatches 47; Indels 22; Gaps 8.

QY 7 LVLILL----FWIPVSGDVTYQPLSLPVFPGDVSISCSOSSISLAKSYGNTLYSYL 62
      ||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 15 LILCLILSLASCFCTGATGTEVKYTOPEKSYSAAGDSTILNCTVTSILPVG----PIRW- 70
      |||:|||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 63 HKPGSGPOLLITYGISN----RESGVPDRSSGSGSDTFLKSTIKPEDLGMYCL--Q 115
      |||:|||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 70 RGVGGS-RLIYSFTGEHPRVRYNSD--TKRNNMADFIRISNVPEDAGTYCYVKFOR 126
      |||:|||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 116 GTHQPYT---FGGCKLEI 131
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 127 GSSEPDTEIOSGGTEVYV 145
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

RESULT 6
ID 088555 PRELIMINARY; PRT; 509 AA.
AC 088555;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE INHIBITORY RECEPTOR SHPS-1 LONG ISOFORM.
DE SHPS1.
GN MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCUROGNATHI; MORIDA; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6; TISSUE-THYMUS;

```

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RA VEILLETTE A., THIBAUDEAU E., LATOUR S.;  
RT "High expression of inhibitory receptor SHS-1 and its association  
RL with protein tyrosine phosphatase SHP-1 in macrophages.";  
R J. BIOL. CHEM. 0:0-0(1998).  
DR EMBL; AF072543; G3273916; -.  
SQ SEQUENCE 509 AA; 55986 MW; 34FB651 CRC32;
```

Query Match 19.7%; Score 137; DB 10; Length 509;
Best Local Similarity 31.4%; Pred. No. 2e-05;
Matches 44; Conservative 25; Mismatches 47; Indels 24; Gaps

Dt 7 LTVLL-----FWIVSGGDVVYTOTPLSLPVSPFGQVSISSRSSGLAKSYGNTLYSWYL 62
Db 15 LCLILLASACCTCATGATKELKVTOPEKSVSAAGSTVLNCTLSLPVG---PIRWY- 70
Qy 63 HKPGSP-QLLIYGISN----FSGVPDRFGSGSGDTFTLKISTIKPEDIGMYCL--- 115
Db 70 --RGVGPRLLIYSFAGYVPRIRNVSD--TTKRNMDFSRISNVTPADAGITCYCAFKQ 125
Qy 115 QGTROPYT---FGGGTKLEI 131
Db 126 KGSSEPDTEIQGGGTVEYV 145

RESULT 7
088556 PRELIMINARY; PRT; 291 AA.
088556:
AC 088556;
DT 01-NOV-1998 (TREMBLREL_08, CREATED)
DT 01-NOV-1998 (TREMBLREL_08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL_08, LAST ANNOTATION UPDATE)
DE INHIBITORY RECEPTOR SHPS-1 SHORT ISOFORM.
GN SHPS1.
OS MUS MUSCULUS (MOUSE).
OC EKARROTA; METAFAA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CC RODENTIA; SCURIOGNATHI; MORIDAE; MORINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=THYMUS;
RA VEILLETTE A., THIBAUDEAU E., LATOUR S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RL with protein tyrosine phosphatase SHP-1 in macrophages.";
R J. BIOL. CHEM. 0:0-0(1998).
DR EMBL; AF072544; G3273918; -.
SQ SEQUENCE 291 AA; 31735 MW; CB92D685 CRC32;

Query Match 19.7%; Score 137; DB 10; Length 291;
Best Local Similarity 31.4%; Pred. No. 1.1e-05;
Matches 44; Conservative 25; Mismatches 47; Indels 24; Gaps

Dt 7 LTVLL-----FWIVSGGDVVYTOTPLSLPVSPFGQVSISSRSSGLAKSYGNTLYSWYL 62
Db 15 LCLILLASACCTCATGATKELKVTOPEKSVSAAGSTVLNCTLSLPVG---PIRWY- 70
Qy 63 HKPGSP-QLLIYGISN----FSGVPDRFGSGSGDTFTLKISTIKPEDIGMYCL--- 115
Db 70 --RGVGPRLLIYSFAGYVPRIRNVSD--TTKRNMDFSRISNVTPADAGITCYCAFKQ 125
Qy 115 QGTROPYT---FGGGTKLEI 131
Db 126 KGSSEPDTEIQGGGTVEYV 145

RESULT 8
015533 PRELIMINARY; PRT; 50 AA.
015533:
AC 015533;
DT 01-NOV-1996 (TREMBLREL_01, CREATED)
DT 01-NOV-1996 (TREMBLREL_01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL_08, LAST ANNOTATION UPDATE)
DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA

KM SIGNAL; TRANSMEMBRANE; ALTERNATIVE SPLICING; IMMUNOGLOBULIN FOLD;
KW GLYCOPROTEIN; SH3-BINDING; PHOSPHORYLATION.
FT SIGNAL 1 26
FT CHAIN 27 509
FT DOMAIN 28 373
FT TRANSFER 374 394
FT DOMAIN 395 509
FT DOMAIN 51 125
FT DOMAIN 168 234
FT DOMAIN 270 336
FT DOMAIN 436 439
FT DOMAIN 446 451
FT DOMAIN 460 463
FT DOMAIN 477 480
FT DOMAIN 501 504
FT MOD_RES 436 436
FT MOD_RES 460 460
FT MOD_RES 477 477
FT MOD_RES 501 501
FT CARBOHYD 54 54
FT CARBOHYD 93 93
FT CARBOHYD 169 169
FT CARBOHYD 181 181
FT CARBOHYD 203 203
FT CARBOHYD 209 209
FT CARBOHYD 242 242
FT CARBOHYD 246 246
FT CARBOHYD 271 271
FT CARBOHYD 293 293
FT CARBOHYD 312 312
FT CARBOHYD 320 320
FT CARBOHYD 345 345
FT CONFLICT 162 162
SQ SEQUENCE 509 AA; 55690 MM; 6D940097 CRC32; G -> A (IN REF. 2 AND 3).

Query Match 17.2%; Score 119.5; DB 10; Length 509;
Best Local Similarity 30.4%; Pred. No. 0.00086;
Matches 42; Conservative 22; Mismatches 55; Indels 19; Gaps 7;

QY 7 LVLVLL---FWIPVSGDVVVTQPLSLPVSFGDQVSISSRSOSLAKSYGNTYLSMYL 62
DB 15 LFCILLASCFACAGASGKELKVTQADKSVSAAGDSATLNCYSLTPVG---PIKWK 70
QY 63 HK-PGOSPOLLITIGISN--RPSGVDPDRFSGSGGTFTLKISTIKPEDLGMYYCL---QG 116
DB 71 GEGONRSPPIYSFISGHEHPRITNVS--ATKRNMDPISICISNVTPEAGTYCYVKFKG 128
QY 117 THOPTY---FGGKLEI 131
DB 129 IVEPTEIKSGGGTTLTV 146

RESULT 15
070426 PRELIMINARY; PRT; 418 AA.
ID 070426
AC 070426
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SIGNAL REGULATORY PROTEIN ALPHA (FRAGMENT).
OS RATIUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATIUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WAG/RIJ;
RA ADAMS S., VAN DER LAAN L.J.W., VERNON-WILSON E.,
RA RENARDEL DE LAVALLETTE C., DOPP E.A., DIKSTRA C., SIMMONS D.L.,
RA VAN DEN BERG T.K.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF055065; G3170529; --
FT NON_TER 418 418

SQ SEQUENCE 418 AA; 45297 MM; 752D2171 CRC32;

Query Match 16.6%; Score 115.5; DB 10; Length 418;
Best Local Similarity 29.7%; Pred. No. 0.0017;
Matches 41; Conservative 24; Mismatches 54; Indels 19; Gaps 7;

QY 7 LVLVLL---FWIPVSGDVVVTQPLSLPVSFGDQVSISSRSOSLAKSYGNTYLSMYL 62
DB 14 LFCILLASCFACAGASGKELKVTQADKSVSAAGDSATLNC---TVCSLTPVGPIKWK 69
QY 63 HK-PGOSPOLLITIGISN--RPSGVDPDRFSGSGGTFTLKISTIKPEDLGMYYCL---QG 116
DB 70 GEGONRSPPIYSFISGHEHPRITNVS--ATKRNMDPISICISNVTPEAGTYCYVKFKG 127
QY 117 THOPTY---FGGKLEI 131
DB 128 IVEPTEIKSGGGTTLTV 145

Search completed: May 11, 1999, 12:21:01
Job time: 253 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 11:39:53 ; Search time 44.09 Seconds

(Without alignments)
60.552 Million cell updates/sec

Title: us-08-700-737-12

Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CIQGTHTPTTGGGKLEIK 132

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database: A_Geneseq_34.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	695	100.0	132	1	W53814	Murine Act-1 light
2	695	100.0	140	1	W53817	Consensus protein
3	608	87.5	138	1	W53812	Light chain of a h
4	559.5	80.5	238	1	W14942	3F4 Human IgG4 exp
5	559.5	80.5	238	1	W14937	Murine anti-porcine
6	558.5	80.4	131	1	W34518	Variable kappa cha
7	554.5	79.8	149	1	W03199	Anti-Idiotypic mono
8	548.5	78.9	131	1	R52772	Murine KC-4 immuno
9	548.5	78.9	131	1	R52790	Murine KC-4 immuno
10	548.5	78.9	131	1	R70457	VL sequence of ant
11	543.5	78.2	131	1	R32451	Chimeric Mab light
12	543.5	78.2	131	1	R31587	BES-2 light chain
13	537.5	77.3	131	1	R32245	BES-2 murine IgG3
14	537.5	77.3	131	1	R52822	Humanised murine K
15	537.5	77.3	131	1	R70470	Humanised anti-KC-
16	535.5	77.1	238	1	W31752	L chain subunit of
17	535.5	77.1	132	1	W60867	Variable region of
18	535.5	77.1	238	1	W71889	Anti-human Fas mon
19	529.5	76.2	140	1	W68492	Variable light cha
20	527.5	75.9	172	1	R15199	R6-5-D6 anti-ICAM-
21	523	75.3	150	1	R11598	Murine monoclonal
22	519.5	74.7	131	1	R52788	Murine BRE-3 immu
23	519.5	74.7	131	1	R52770	Murine BRE-3 immu
24	517.5	74.5	131	1	R09424	Co-1 Light Chain V
25	517.5	74.5	131	1	W06214	Mab Co-1 light cha
26	513	73.8	127	1	W76124	Murine ICR-8.1 V-K
27	513	73.8	127	1	W71254	Murine antibody IC
28	511.5	73.6	131	1	R52806	Humanised murine B
29	509	73.2	132	1	W50219	Amino acid sequenc
30	506.5	72.9	173	1	R15059	Murine anti-ICAM m
31	503	72.4	239	1	W71876	Anti-human Fas hum
32	503	72.4	239	1	W71878	Anti-human Fas hum
33	500	71.9	239	1	W71887	Anti-Fas Mab CH11
34	499	71.8	239	1	W71879	Anti-human Fas hum
35	499	71.8	239	1	W71879	Anti-human Fas hum
36	495	71.2	249	1	R21262	pSCFVNO11 encoding
37	489	70.4	249	1	P80154	Biosynthetic antib
38	488.5	70.3	219	1	R56235	h66-118/h13-65/11-
39	485	69.8	135	1	R54052	Sequence of the VL
40	485	69.8	135	1	W01525	Monoclonal antibody
41	485	69.8	135	1	W24989	Monoclonal antibody
42	483	69.2	115	1	P81364	Light chain variab
43	481	69.2	263	1	R15055	Om212 single chain

ALIGNMENTS

44 481 69.2 246 1 R27245 Sequence of the AA
45 481 69.2 110 1 R38159 Sequence of the 11

RESULT 1
ID W53814 W53814 standard; Protein; 132 AA.
AC W53814:
DE 14-JUL-1998 (first entry)
DE Murine Act-1 light chain variable region.
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
OS Mus sp.
FH Key
FT Peptide 1..20 Location/Qualifiers
FT Protein /note="signal peptide"
FT /note="mature protein"
PN W09806248-A2.
PD 19-FEB-1998.
PF 06-AUG-1997; U13884.
PR 15-AUG-1996; US-700737.
PA (LEUK-) LEUKOSITE INC.
PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J;
DR WPI; 98-159172/14.
DR N-PSDB; V20077.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Claim 23; Fig 7; 145pp; English.
CC The present sequence represents the light chain variable region of
CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
CC integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a
CC ligand of this particular integrin. The Act-1 antibody interferes with
CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
CC endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leukocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.
SQ Sequence 132 AA;

Query Match 100.0%; Score 695; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGDVVTQTPLSPYFGQVVISCRSSQSLAKSGYNTLSW 60
|||||
DB 1 MKLPVRLVLLFWIPVSGGDVVTQTPLSPYFGQVVISCRSSQSLAKSGYNTLSW 60
|||||
QY 61 YLHKPGSPOLLTYGISNRSQVDFRFSGGSGTDFLTIKSTIKPEDLGMYYCLOGTHOP 120
|||||
DB 61 YLHKPGSPOLLTYGISNRSQVDFRFSGGSGTDFLTIKSTIKPEDLGMYYCLOGTHOP 120
|||||

QY 121 YTFGGGKLEIK 132
|||||
DB 121 YTFGGGKLEIK 132
|||||

RESULT 2
ID W53817 W53817 standard; Protein; 140 AA.
AC W53817:
DE 14-JUL-1998 (first entry)

DE Consensus protein sequence of the murine variable light chain region.
 KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal addressin cell adhesion molecule-1; MadCAM-1;
 KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease.
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT 1.20
 FT /note="signal peptide"
 FT 21.140
 FT /note="mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendis MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI; 98-159172/14.
 DR N-PSDB; V20086.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3; 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal addressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 140 AA;

Query Match 100.0%; Score 695; DB 1; Length 140;
 Best Local Similarity 100.0%; Pred. No. 1.2e-49;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLPRLVLLLFVIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPRLVLLLFVIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 QY 61 YLHKGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIPEDIGMYTCLOGTHOP 120
 DB 61 YLHKGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIPEDIGMYTCLOGTHOP 120
 QY 121 YTFGGGTRLEIK 132
 DB 121 YTFGGGTRLEIK 132

RESULT 3
 W53812
 ID W53812 standard; Protein; 138 AA.
 AC W53812;
 DT 14-JUN-1998 (first entry)
 DE Light chain of a humanised murine Act-1 antibody.
 KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal addressin cell adhesion molecule-1; MadCAM-1;
 KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;

KM inflammatory bowel disease.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT Protein
 FT 1.20
 FT /note="signal peptide"
 FT 21.138
 FT /note="mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendis MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI; 98-159172/14.
 DR N-PSDB; V20075.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 15; Fig 12; 145pp; English.
 CC The present sequence represents the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal addressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in muscosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 138 AA;

Query Match 87.5%; Score 608; DB 1; Length 138;
 Best Local Similarity 87.1%; Pred. No. 1.2e-42;
 Matches 115; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPRLVLLLFVIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPRLVLLLFVIPVSGGVVYTORPLSPVSGDVSISCRSSOSLAKSYGNTYLSW 60
 QY 61 YLHKGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIPEDIGMYTCLOGTHOP 120
 DB 61 YLHKGSPOLLIIYGISNRFSGVDPDRFSGSGSDFTIKITIPEDIGMYTCLOGTHOP 120
 QY 121 YTFGGGTRLEIK 132
 DB 121 YTFGGGTRLEIK 132

RESULT 4
 W14942
 ID W14942 standard; Protein; 238 AA.
 AC W14942;
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 KM Xenotransplantation; graft rejection; cell interaction; pig;
 KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 PN W09711971-A1.
 PD 03-APR-1997.
 PR 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR N-PSDB; T62938.

PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells
PS Disclosure: Page 65-66; 105pp; English.
CC Heavy chain (W14941) and light chain (W14942) sequences
CC correspond to murine anti-porcine soluble vascular cell adhesion
CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
CC also T62938). A chimeric antibody specific for porcine VCAM can be
CC produced in transfected host cells. It is useful for diagnosing
CC human rejection of porcine xenotransplants and for improving
CC xenotransplantation of porcine cells, tissues and organs into human
CC recipients.
SQ Sequence 238 AA;

Query Match 80.5%; Score 559.5; DB 1; Length 238;
Best Local Similarity 81.1%; Pred. No. 1.7e-38;
Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFQDVVISCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSSSDVVMVMTQPLSLPVSLGDAQASISCRSSQSLVHNSNTYLSW 59
QY 61 YLHKGQSPOLLITIGISNRSFQVDPDRFSGSGGTDFLTIKSTIKPEDLGMVYCLQGTQHP 120
DB 60 YLQKPGQSPKLLITIKVSNRFSQVDPDRFSGSGGTDFLTIKISRAEADLVGYFCQSSTHVP 119
QY 121 YTFGGGTRLEIK 132
DB 120 YTFGGGTRLEIK 131

RESULT 5
W14937
ID W14937 standard: Protein; 238 AA.
AC W14937;
DE 16-JUN-1997 (first entry)
KW Murine anti-porcine VCAM 3F4 light chain.
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
OS Mus sp.
FS Key
FT region Location/Qualifiers
FT region 43..58
FT region /Label= CDR1
FT region 74..80
FT region /Label= CDR2
FT region 113..121
FT region /Label= CDR3
PN MO9711971-A1.
PD 03-APR-1997.
PE 27-SEP-1996; US-55575.
PR 28-SEP-1995; US-004489.
PR 26-SEP-1996; US-004489.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI Rother RP;
DR WPI: 97-212855/19.
DR N-PSDB: T62934
PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells
PS Disclosure: Page 52-53; 105pp; English.
CC Light chain (W14937) and heavy chain (W14938) sequences are
CC provided for the murine anti-porcine soluble vascular cell adhesion
CC molecule (VCAM) monoclonal antibody (Mab) 3F4. Hybridoma 3F4 was
CC produced by standard techniques using recombinant, soluble porcine
CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
CC Mab 3F4 and 2A2 (see also W14931-32) variable regions into
CC expression plasmid pAPEX-3P modified to contain the human gamma4
CC constant region in place of the human gamma1 C1 region. Sequences
CC are provided for 3F4 (chimeric) human G2/G4 cDNA (W14939), a 3F4

CC human G2/G4 expression plasmid insert product (W14940), and 3F4
CC human IgG4 expression plasmid insert products (W14941-42). The
CC chimeric antibodies are specific for porcine VCAM. They are useful
CC for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs
CC into human recipients.
SQ Sequence 238 AA;

Query Match 80.5%; Score 559.5; DB 1; Length 238;
Best Local Similarity 81.1%; Pred. No. 1.7e-38;
Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFQDVVISCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSSSDVVMVMTQPLSLPVSLGDAQASISCRSSQSLVHNSNTYLSW 59
QY 61 YLHKGQSPOLLITIGISNRSFQVDPDRFSGSGGTDFLTIKSTIKPEDLGMVYCLQGTQHP 120
DB 60 YLQKPGQSPKLLITIKVSNRFSQVDPDRFSGSGGTDFLTIKISRAEADLVGYFCQSSTHVP 119
QY 121 YTFGGGTRLEIK 132
DB 120 YTFGGGTRLEIK 131

RESULT 6
W34518
ID W34518 standard: Protein; 131 AA.
AC W34518;
DE 19-MAR-1998 (first entry)
KW Variable kappa chain of antibody from hybridoma 1-706-139.
KW Variable region coding sequence; constant region epitope; hybridoma;
KW antibody detection; antigen/antibody complex; variable heavy chain.
OS Mus musculus.
FS Key
FT region Location/Qualifiers
FT region 31-JUL-1997.
PE 17-JAN-1997; U01074.
PR 23-JAN-1996; US-589939.
PA (ABBO) ABBOTT LAB.
PI Golden AM, Hackett JR, Hoff JA, Ostrow DH;
PI WPI: 97-393833/36.
DR N-PSDB: T98835.
PT Use of antibody constant region epitope(s) - as control or
PT calibrator reagents in assays for detecting the presence of an
PT antibody in a test sample
PS Disclosure: Page 62-63; 109pp; English.
CC This sequence represents the variable kappa chain of the antibody
CC produced by hybridoma 1-706-139, and can be detected using the method of
CC the invention. The method is for detecting the presence of antibody which
CC may be present in a test sample. It comprises contacting a test sample
CC suspected of containing the antibody with an antigen specific for the
CC antibody to allow the formation of antigen/antibody complexes, detecting
CC the presence of the antibody which may be present in the test sample and
CC employing, as a control or calibrator, a reagent which binds to the
CC antigen. The improvement to this method over previous methods, comprises
CC employing, as the control or calibrator, a reagent comprising one or more
CC antibody constant region epitopes, where the reagent binds to the antigen
CC and is homogeneous with respect to specificity and affinity. The method
CC can also be used for detecting the presence of antibodies developed
CC against more than one antigen. The method is used particularly for the
CC detection of human antibodies specific for a given antigen, e.g. HIV-1,
CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
CC of the problems associated with using an immune sera in the manufacture
CC of calibrators and positive controls. The present reagents can be readily
CC and reproducibly generated in virtually unlimited quantities and are also
CC useful for quantitating, and monitoring the integrity of, the antigen
SQ Sequence 131 AA;

Query Match 80.4%; Score 558.5; DB 1; Length 131;
Best Local Similarity 81.1%; Pred. No. 1.1e-38;

Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVTOTPLSPVSGDVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGDVTOTPLSPVSGDVISCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLITVIGINRSGVDPDRFSGSGGDTFTLKISTIKPELGMVYCLQGTROP 120
 DB 60 YLQKPGSPOLLITVIGINRSGVDPDRFSGSGGDTFTLKISTIKPELGMVYCLQGTROP 119

QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 7
 W03199
 ID W03199 standard; Protein: 149 AA.
 AC W03199;
 DT 26-FEB-1997 (first entry)
 DE Anti-idiotype monoclonal antibody 1A7 variable light chain.
 KW Murine; mouse; anti-idiotype; monoclonal antibody; Mab; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 KW amplification; gene therapy.
 OS Mus musculus.

FT Key Location/Qualifiers
 FT peptide 1..19
 FT region /label= sig_peptide
 FT region /note= "framework region 1"
 FT region 43..58
 FT region /note= "complementarity determining region 1"
 FT region 59..73
 FT region /note= "framework region 2"
 FT region 74..80
 FT region /note= "complementarity determining region 2"
 FT region 81..112
 FT region /note= "framework region 3"
 FT region 113..121
 FT region /note= "complementarity determining region 3"
 FT region 122..131
 FT region /note= "framework region 4"

PN W09622373-A2.
 PD 25-JUL-1996.
 PF 17-JAN-1996; U00882.
 PR 17-JAN-1995; US-372676.
 PR 16-JAN-1996; US-372676.
 PA (KENT) UNIV KENTUCKY.
 PI Chatterjee M., Chatterjee SK, Foon KA;
 DR WPI: 96-354530/35.
 DR N-PSDB; T31332.
 FT Monoclonal antibody 1A7 and related polynucleotide(s) and
 FT polypeptide(s) - useful to treat or palliate a GD2-associated
 FT disease, e.g. melanoma and glioma
 PS Claim 8; Fig 1; 141pp; English.
 CC The present sequence is that of the murine anti-idiotype monoclonal
 CC antibody (Mab) 1A7 variable light chain. Mab 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) Mab 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC Mab 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or

CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 SQ Sequence 149 AA;

Query Match 79.8%; Score 554.5; DB 1; Length 149;
 Best Local Similarity 79.5%; Pred. No. 2,7e-38;
 Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVTOTPLSPVSGDVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGDVTOTPLSPVSGDVISCRSSQSLAKSYGNTYLSW 59

QY 61 YLHRPGSPOLLITVIGINRSGVDPDRFSGSGGDTFTLKISTIKPELGMVYCLQGTROP 120
 DB 60 YLQKPGSPOLLITVIGINRSGVDPDRFSGSGGDTFTLKISTIKPELGMVYCLQGTROP 119

QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 8
 R52772
 ID R52772 standard; Protein: 131 AA.
 AC R52772;
 DT 24-JAN-1995 (first entry)
 DE Murine KC-4 immunoglobulin light chain variable region (deduced).
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human milk fat globule; human breast carcinoma;
 KW murine anti-human carcinoma monoclonal antibody KC-4.
 OS Mus musculus.

FT Key Location/Qualifiers
 FT protein 20..131
 FT region /label= KC-4_mature_VL-chain
 FT region 20..42
 FT region /label= FRL
 FT region 43..58
 FT region /label= CDRI
 FT region 59..73
 FT region /label= FR2
 FT region 74..80
 FT region /label= CDR2
 FT region 81..112
 FT region /label= FR3
 FT modified_site 98..100
 FT region /note= "putative glycosylation site"
 FT region 113..121
 FT region /label= CDR3
 FT region 122..131
 FT region /label= FR4

PN W09411508-A.
 PD 26-MAY-1994.
 PF 15-NOV-1993; U11316.
 PR 13-NOV-1992; US-977706.
 PR 13-NOV-1992; US-977707.
 PR 28-SEP-1993; US-128015.
 PA (CANC) CANCER RES FUND CONTRA COSTA.
 DR WPI: 94-183509/22.
 DR N-PSDB; Q62763.
 FT Chimeric human-murine polypeptide(s) specific for human mammary
 FT fat globule antigen - for imaging, diagnosing and treating
 FT neoplasia, with less undesirable immunogenic response
 PS Example 27; Page 41; 54pp; English.
 CC An initial isolation of cDNAs coding for murine anti-human breast
 CC carcinoma Mab KC-4 was performed using PCR with commercially
 CC available primers (see 062751-062758, available from NOVAGEN).
 CC Subsequent cloning using PCR primers J020, J021, J022 and J024
 CC (see 062759-062762) resulted in the isolation of the mouse Ig
 CC variable domains. The amplified cDNAs were sequenced (062763 and

CC Q62764) and amino acid sequences were deduced from them. Chimeric
 CC mouse-human antibodies were constructed using human constant
 CC regions so as to produce less immunogenic polypeptides which
 CC retained the anti-human carcinoma binding specificity of KC-4.
 SQ Sequence 131 AA;

Query Match 78.9%; Score 548.5; DB 1; Length 131;
 Best Local Similarity 78.8%; Pred. No. 7.2e-38;
 Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDVVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLV-LMFVWPASSSDVLTMTQPLSLPVSLGDAQSISCRSSQSLIYHSGNNTYLEW 59
 QY 61 YLHKPGSPOLLTYIGISNRFSGVDPDRFSGSGSTDTFTLKISTIKPEDLGMVYCLGTHOP 120
 DB 60 YLQKPGSPRLILTYKYSIRSGVDPDRFSGSGSTDTFTLINSRVAEDLGITYCFQGSHP 119
 QY 121 YTFGGGTKLEIK 132
 DB 120 YTFGGGTKLEIK 131

RESULT 9
 ID R52790 standard; Protein; 131 AA.
 AC R52790;
 DT 24-JAN-1995 (first entry)
 DE Murine KC-4 immunoglobulin light chain variable region (deduced).
 KW Immunoglobulin variable domain; primer: polymerase chain reaction;
 KM Chimeric antibody; human milk fat globule; human breast carcinoma;
 OS murine anti-human carcinoma monoclonal antibody KC-4.
 FH Key location/Qualifiers
 FT protein 20..131
 FT /label= KC-4-mature-VL-chain
 FT region 20..42
 FT /label= FR1
 FT region 43..58
 FT /label= CDR1
 FT region 59..73
 FT /label= FR2
 FT region 74..80
 FT /label= CDR2
 FT region 81..112
 FT /label= FR3
 FT modified_site 98..100
 FT /note= putative glycosylation site*
 FT region 113..121
 FT /label= CDR3
 FT region 122..131
 FT /label= FR4
 PN W09411509-A.
 PD 26-MAY-1994.
 PE 16-NOV-1993; U11445.
 PR 16-NOV-1993; US-977696.
 PR 30-SEP-1993; US-129930.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 PI Ceriani RL, Do Couto JJR, Padian EA, Peterson JA;
 DR WPI; 94-183510/22.
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms
 PS Example 26; Page 61; 109pp; English.
 CC An initial isolation of cDNAs coding for murine anti-human breast
 CC carcinoma MAb KC-4 was performed using PCR with commercially
 CC available primers (see Q62776-Q62783, available from NOVAGEN).
 CC Subsequent cloning using PCR primers J020, J021, J022 and J024
 CC (see Q62784-Q62787) resulted in the isolation of the mouse Ig
 CC variable domains. The amplified cDNAs were sequenced (Q62788 and
 CC Q62789) and amino acid sequences were deduced from them. Chimeric

CC mouse-human antibodies were constructed using human constant
 CC regions so as to produce less immunogenic polypeptides which
 CC retained the anti-human carcinoma binding specificity of KC-4.
 SQ Sequence 131 AA;

Query Match 78.9%; Score 548.5; DB 1; Length 131;
 Best Local Similarity 78.8%; Pred. No. 7.2e-38;
 Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDVVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLV-LMFVWPASSSDVLTMTQPLSLPVSLGDAQSISCRSSQSLIYHSGNNTYLEW 59
 QY 61 YLHKPGSPOLLTYIGISNRFSGVDPDRFSGSGSTDTFTLKISTIKPEDLGMVYCLGTHOP 120
 DB 60 YLQKPGSPRLILTYKYSIRSGVDPDRFSGSGSTDTFTLINSRVAEDLGITYCFQGSHP 119
 QY 121 YTFGGGTKLEIK 132
 DB 120 YTFGGGTKLEIK 131

RESULT 10
 ID R70457 standard; Peptide; 131 AA.
 AC R70457;
 DT 27-OCT-1995 (first entry)
 DE VL sequence of anti-KC-4 monoclonal antibody (X11-XK2).
 KW Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
 OS Synthetic.
 PN W09510776-A.
 PD 20-APR-1995.
 PE 16-NOV-1993; U11444.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 PI Ceriani RL, Docouto JJR, Peterson JA;
 DR N-PSDB; 087531.
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Example; Table 14, Page 31; 61pp; English.
 CC The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
 CC were prepared by PCR from polyadenylated RNA isolated from 100
 CC million KC-4 hybridoma cells. All clones were obtained from independent
 CC PCR. The sequences of the primers are given in Q87519-Q87526.
 CC The PCR products were cloned, without prior purification, into pCR1000
 CC (Invitrogen) and sequenced in both directions. The VL DNA sequence and
 CC its derived protein sequences are shown in Q87531 and R70449-R70457.
 CC The mature VL chain begins at AA D of framework 1 (FR1). VL is a
 CC group II kappa chain. Part of the CDR3 and all of the FR4 are
 CC encoded by JK2. There is an asparagine glycosylation site in the
 CC light chain in FR3. The site reads NIS. R70457 is a composite
 CC sequence of R70449-R70456.
 SQ Sequence 131 AA;

Query Match 78.9%; Score 548.5; DB 1; Length 131;
 Best Local Similarity 78.8%; Pred. No. 7.2e-38;
 Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSPFGDVVISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLV-LMFVWPASSSDVLTMTQPLSLPVSLGDAQSISCRSSQSLIYHSGNNTYLEW 59
 QY 61 YLHKPGSPOLLTYIGISNRFSGVDPDRFSGSGSTDTFTLKISTIKPEDLGMVYCLGTHOP 120
 DB 60 YLQKPGSPRLILTYKYSIRSGVDPDRFSGSGSTDTFTLINSRVAEDLGITYCFQGSHP 119
 QY 121 YTFGGGTKLEIK 132
 DB 120 YTFGGGTKLEIK 131

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 59
 QY 61 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
 DB 60 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
 QY 121 YTFGGGSKLEIK 132
 DB 120 YTFGGGSKLEIK 131
 RESULT 13
 R32245
 ID R32245 standard; Protein: 131 AA.
 AC R32245; (first entry)
 DT 09-JUN-1993
 DE BR55-2 murine IgG3 light chain variable domain.
 KW Monoclonal; antibody; MAb; light; heavy; chain; variable; region;
 KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
 KW expression vector; IgG1; IgG3; pV; pVg3; gamma; kappa; constant;
 KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
 KW antigen; Y 6; B-7-2; binding specificity; erythrocyte; diagnosis;
 KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;
 KW gastric; small cell lung; immunotherapy; HIV.
 OS Mus musculus.
 FH Key
 FT protein Location/Qualifiers
 FT 20..131
 FT /note="Mature protein"
 FT region 43..58
 FT /label= CDR1
 FT region 74..80
 FT /label= CDR2
 FT 113..121
 FT /label= CDR3
 FT region
 PN EP-528767-A.
 PD 24-FEB-1993.
 PF 18-AUG-1992; 810633.
 PR 21-AUG-1991; GB-018013.
 PR 02-MAR-1992; GB-004514.
 PA (SANO) SANDOZ LTD.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 PI Co MS, Iolbner H;
 PI WPI: 93-060580/08.
 DR N-PSDB: Q36534.
 PT Human-mouse chimeric monoclonal antibodies - recognise difucosyl
 PT Lewis blood group antigens Y-6 and B-7-2, useful for treating
 PT cancer and HIV infection
 PS Disclosure: Fig 3: 65pp; English.
 CC The sequences given in R32245-46 represent the light and heavy chain
 CC variable regions respectively from the murine monoclonal (MAb) BR55-2
 CC 1993. BR55-2 was used as a basis for the construction of a chimeric
 CC MAb which recognises the difucosyl Lewis blood group. Separate
 CC expression vectors were used to express the chimeric human BR55-2 IgG1
 CC and IgG3 antibody light and heavy chains: pV for the light chain, pVg
 CC for the gamma 1 heavy chain and pVg3 for the gamma 3 heavy chain. The
 CC actual expressed chimeric BR55-2 light chain gene and the heavy chain
 CC gene consist of two adjacent parts. The kappa/gamma constant regions
 CC were built into the vectors pV and pVg3 (or pVg3c) respectively and
 CC the variable regions were constructed by PCR. The resulting plasmids
 CC were used to transfect the host cell line sp2/O-Ag 14 by electro-
 CC poration. The resulting Mabs recognise the difucosyl Lewis blood
 CC group antigens Y-6 and B-7-2 but do not induce human anti-mouse anti-
 CC body response. The Mabs show a restricted binding specificity which is
 CC associated with a lack of cross-reactivity to related antigens
 CC expressed on blood cells eg. erythrocytes. This allows the Mabs to be
 CC particularly useful for therapeutic use in humans. The Mabs are
 CC useful in the diagnosis and treatment of cancer of epithelial origin,
 CC eg. breast, colorectal, ovarian, prostate, pancreatic or gastric
 CC cancer and small cell lung cancer. The Mabs are also useful for

CC Immunotherapy of HIV infections since the Lewis Y antigen is also
 CC selectively expressed on HIV infected cells.
 SQ Sequence 131 AA;

Query Match 77.3%; Score 537.5; DB 1; Length 131;
 Best Local Similarity 77.3%; Pred. No. 5, 6e-37;
 Matches 102; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 59
 QY 61 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
 DB 60 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
 QY 121 YTFGGGSKLEIK 132
 DB 120 YTFGGGSKLEIK 131

RESULT 14
 R52822
 ID R52822 standard; Protein: 131 AA.
 AC R52822;
 DT 25-JAN-1995 (first entry)
 DE Humanised murine KC-4 immunoglobulin light chain V-region.
 KW Immunoglobulin variable domain; primer; polymerase chain reaction;
 KW chimeric antibody; human mammary fat globule; human breast carcinoma;
 KW murine anti-HMFg monoclonal antibody KC-4; humanised analogue.
 OS Chimeric Mus musculus.
 PN MO9411509-A.
 PD 26-MAR-1994.
 PF 16-NOV-1993; U11445.
 PR 16-NOV-1992; US-977696.
 PR 30-SEP-1993; US-129930.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
 DR WPI: 94-183510/22.
 DR N-PSDB: Q62803.
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms
 PS Example 75: Page 95; 109pp; English.
 CC This sequence represents a humanised murine anti-human carcinoma
 CC KC-4 antibody light chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.
 SQ Sequence 131 AA;

Query Match 77.3%; Score 537.5; DB 1; Length 131;
 Best Local Similarity 77.3%; Pred. No. 5, 6e-37;
 Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGDVVVTQPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 59
 QY 61 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 120
 DB 60 YLHKPQSPQLLYIGISNRFSGVDPDRFSGSGSTDTFLKISTIKPDLGMYCYLQGTROP 119
 QY 121 YTFGGGSKLEIK 132
 DB 120 YTFGGGSKLEIK 131

RESULT 15

R70470
 ID R70470 standard; Protein; 131 AA.
 AC R70470; ~~_____~~
 DT 27-OCT-1995 (first entry)
 DE Humanised anti-KC-4 antibody VL FR-H2.
 KW Anti-KC-4 antibody; humanised antibody; cancer.
 OS Synthetic.
 PN WO9510776-A.
 PD 20-APR-1995.
 PE 16-NOV-1993: U11444.
 PR 08-OCT-1993: US-134346.
 PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 PI Ceriani RL, Docuto JJR, Peterson JA;
 DR WPI; 95-161912/21.
 DR N-PSDB; Q87533.
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells. In vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Claim 2; Table 24, page 51; 61pp; English.
 CC Hybridomas were prepd. based on the anti-KC-4 mouse hybridoma ATCC
 CC HB 8710 (US4708930). The murine variable regions were modified at
 CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
 CC humanised DNA sequences for the VH and VL segments are shown in
 CC Q87534 and Q87533 respectively. Plasmid constructions comprising
 CC the humanised variable regions and the human constant regions were
 CC then used to transform SSP2/0-Ag14 myeloma cells to produce the
 CC humanised anti-KC-4 Mabs. The deduced AA sequences of the
 CC humanised anti-KC-4 variable light and heavy chains are given in
 CC R70470 and R70471 respectively.
 SQ Sequence 131 AA;

Query Match 77.3%; Score 537.5; DB 1; Length 131;
 Best Local Similarity 77.3%; Pred. No. 5.6e-37;
 Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLEPVRLVLLLEWIPVSGDVVVTQTPLSLPVSEGDVVISCRSSQSLAKSYGNTYLSW 60
 Db 1 MKLEPVRLVLLLEWIPVSGDVVVTQTPLSLPVSEGDVVISCRSSQSLAKSYGNTYLSW 59
 QY 61 YLHPPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFLTIKSTIKPEDIGMYTCLGTHOP 120
 Db 60 YLQPPGSPOLLITIKVSVIRFSGVDPDRFSGSGGTDFLTIKSVREAEVGYTCFQGSHP 119
 QY 121 YTFGGTKLEIK 132
 Db 120 YTFGGTKLEIK 131

Search completed: May 11, 1999, 12:14:53
 Job time: 2100 sec

Description

Source

/organism="unidentified"

BASE COUNT 401 a 465 c 378 g 328 t
ORIGIN

Query Match 80.0%; Score 335.8; DB 6; Length 1572;
Best Local Similarity 87.6%; Pred. No. 2.1e-95;
Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCCTCTCTCTGATATCAACAGCTCAAGTCCACCTCCAG 60
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49 ATGGGATGGAGCTGATATCCTCTCTCTGATATCAACAGCTCAAGTCCACCTCCAG 108
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61 GTCCACATCAGCAGCCTGGGCTGAGCTTGTGAAGCCTGGGACCTCACTGAGAGCTGCC 120
|||||
109 GTCCACATCAGCAGCCTGGGCTGAGCTTGTGAAGCCTGGGACCTCACTGAGAGCTGCC 168
|||||
121 TGCAGAGGTTATGCTTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 180
|||||
169 TGCAGAGGTTATGCTTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 228
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181 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 240
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229 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 288
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241 CAAAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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289 GAGAGGTTCAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348
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301 CAGCTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
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349 CAACTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 408
|||||
361 GAGGATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
|||||
409 TATGCTTACGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
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RESULT 2
LOCUS 164458 1572 bp DNA PAT 26-SEP-1997
DEFINITION Sequence 23 from patent US 5665357.
ACCESSION 164458
NID 92481352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1572)
AUTHORS Rose, M. Samuel, Boot, C., Copley, C., Graham, Paterson, D. Stephen,
Hall, S. Margaret, Wright, A. Firman and Blakey, D. Charles.
TITLE Antibodies recognizing tumor associated antigen CA 55.1
JOURNAL Patent: US 5665357-A 23 09-SEP-1997;
FEATURES
source 1.1572
/organism="unknown"
BASE COUNT 401 a 465 c 378 g 328 t
ORIGIN

Query Match 80.0%; Score 335.8; DB 6; Length 1572;
Best Local Similarity 87.6%; Pred. No. 2.1e-95;
Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCCTCTCTCTGATATCAACAGCTCAAGTCCACCTCCAG 60
|||||
49 ATGGGATGGAGCTGATATCCTCTCTCTGATATCAACAGCTCAAGTCCACCTCCAG 108
|||||
61 GTCCACATCAGCAGCCTGGGCTGAGCTTGTGAAGCCTGGGACCTCACTGAGAGCTGCC 120
|||||
109 GTCCACATCAGCAGCCTGGGCTGAGCTTGTGAAGCCTGGGACCTCACTGAGAGCTGCC 168
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121 TGCAGAGGTTATGCTTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 180
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169 TGCAGAGGTTATGCTTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 228
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181 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 240
|||||
229 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 288
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241 CAAAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
|||||
289 GAGAGGTTCAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348
|||||
301 CAGCTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
|||||
349 CAACTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 408
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361 GAGGATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
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409 TATGCTTACGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
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|||||
DB 169 TGCAGAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 228
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DB 181 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 240
|||||
DB 229 GGACAGGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 288
|||||
DB 241 CAAAATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
|||||
DB 289 GAGAGGTTCAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 348
|||||
DB 301 CAGCTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
|||||
DB 349 CAACTCAGCAGCCTGATCATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 408
|||||
DB 361 GAGGATGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
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DB 409 TATGCTTACGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
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RESULT 3
LOCUS 571019 446 bp mRNA ROD 22-SEP-1994
DEFINITION IgG1-anti-erbB-2 product monoclonal antibody heavy chain variable
region [mice, E401 hybridoma, mRNA partial, 446 nt].
ACCESSION 571019
NID 9546187
KEYWORDS
SOURCE Mus sp. E401 hybridoma.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 446)
AUTHORS Ishida, T., Tsujisaki, M., Hinoda, Y., Imai, K. and Yachi, A.
TITLE Establishment and characterization of mouse-human chimeric
monoclonal antibody to erbB-2 product
Jpn. J. Cancer Res. 85 (2), 172-178 (1994)
JOURNAL 94193471
MEDLINE
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI g1dbsq 149475] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
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/note="anti-erbB-2 product monoclonal antibody heavy chain
variable region"
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1.444
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/note="This sequence comes from Fig. 2. Protein sequence
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mismatches([I->T],63[Q->G])"
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/product="anti-erbB-2 product monoclonal antibody heavy
chain variable region"
/db_xref="PDB:9546188"
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QLSTSEDAVYICAREYTDGYEDDYDGOGTTLVSSGSKSPV"

BASE COUNT 114 a 117 c 117 g 98 t
ORIGIN

Query Match 79.8%; Score 335.2; DB 13; Length 446;
Best Local Similarity 87.4%; Pred. No. 2.8e-95;
Matches 367; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

1 ATGGGATGGAGCTGATATCCTCTCTCTGATATCAACAGCTCAAGTCCACCTCCAG 60
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Db 7 ATGGGATGGAGCTGGATGCTTTCTTTTGGTGGCAACACTACAGATGTCCACTCCAG 66...
QY 61 GTCCAACTGCAGAGCCTGGGGCTGAGCTGTGAAGCCTGGGACTTCAGTAAGCTGTCC 120
Db 67 GTCCAACTGCAGAGCCTGGGGCTGAGCTGTGAAGCCTGGGACTTCAGTAAGCTGTCC 126
QY 121 TGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 180
Db 127 TGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 186
QY 181 GGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 240
Db 187 GGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 246
QY 241 CAAAATTCAGAGGCAAGGCAAGCATTGACTGTGACATTCCTCCAGCAGAGCCTCATG 300
Db 247 GAGAAATTCAGAGGCAAGGCAAGCATTGACTGTGACATTCCTCCAGCAGAGCCTCATG 306
QY 301 CAGCTCAGAGCCTGACATCTGAGACTCTGCGTCTACTATTGTGCAAGAGGGGTTAC 360
Db 307 CAGCTCAGAGCCTGACATCTGAGACTCTGCGTCTACTATTGTGCAAGAGAGACTAT 366
QY 361 GAGGATGGGACTATGCTATGCTACTGCGGTGCAAGGCAAGCCTGACCTCTCTCTCA 420
Db 367 GATGGTACTACGAGGACTTGTGACTGTGGGCCAAGGCAAGCCTGACCTCTCTCTCA 426

RESULT 4
AF045500 417 bp mRNA ROD 28-FEB-1998
LOCUS Mus musculus 4B8 monoclonal antibody heavy chain variable region,
DEFINITION (IGH) mRNA, partial cds.
ACCESSION AF045500
KEYWORDS 92906083
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 417)
AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollner, B.D.
TITLE Anti-DNA antibodies of normal mice immunized with poly(dC) are
structurally similar to natural autoantibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 417)
AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollner, B.D.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
FEATURES
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/strain="C57BL/6"
/db_xref="taxon:10090"
/cell_line="spleen cell hybridoma"
/chromosome="12"
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GYTFTSYMMHWKQRPQGLIEWIGVIDPSDSTYNQKGRATLVDSSTAVWOL
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BASE COUNT 96 a 107 c 116 g 98 t
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Query Match 79.4%; Score 333.6; DB 13; Length 417;
Best Local Similarity 88.8%; Pred. No. 8.8e-95;
Matches 373; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 ATGGGATGGAGCTGTATCATTCCTTGTGTGTAACAAGCTACAGTGTCCACTCCAG 60
Db 1 ATGGGATGGAGCTGTATCATTCCTTGTGTGTAACAAGCTACAGTGTCCACTCCAG 60
QY 61 GTCCAACTGCAGAGCCTGGGGCTGAGCTGTGAAGCCTGGGACTTCAGTAAGCTGTCC 120
Db 61 GTCCAACTGCAGAGCCTGGGGCTGAGCTGTGAAGCCTGGGACTTCAGTAAGCTGTCC 120
QY 121 TGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 180
Db 121 TGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 180
QY 181 GGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 240
Db 181 GGCAGAGGCTTATGCTACACCTTCACCACTGACTGTGACATGCGTGAAGCAGAGGCT 240
QY 241 CAAAATTCAGAGGCAAGGCAAGCATTGACTGTGACATTCCTCCAGCAGAGCCTCATG 300
Db 241 CAAAATTCAGAGGCAAGGCAAGCATTGACTGTGACATTCCTCCAGCAGAGCCTCATG 300
QY 301 CAGCTCAGAGCCTGACATCTGAGACTCTGCGTCTACTATTGTGCAAGAGGGGTTAC 360
Db 301 CAGCTCAGAGCCTGACATCTGAGACTCTGCGTCTACTATTGTGCAAGAGGGGTTAC 360
QY 361 GAGGATGGGACTATGCTATGCTACTGCGGTGCAAGGCAAGCCTGACCTCTCTCTCA 420
Db 358 CTCCTCAGGCTACGAGAGGTTGCTTACTGTGGGCCAAGGCAAGCCTGCTCTCTCTCA 417

RESULT 5
MUSIGKCLP 462 bp mRNA ROD 15-DEC-1988
LOCUS Mouse Igmk rearranged heavy-chain mRNA variable region (V-D-J)
DEFINITION anti-DNA autoantibody.
ACCESSION M20835
KEYWORDS 9196945
SOURCE V-region; autoantibody; immunoglobulin heavy chain.
ORGANISM Mouse (Strain MRL-Mp -1Pr/1Pr) spleen hybridoma cell line
MRL-DNA22, cDNA to mRNA.
Eukaryota; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Kofler, R., Strohal, R., Balders, R.S., Johnson, M.E., Noonan, D.J.,
Duchosal, M.A., Dixon, F.J. and Theofilopoulos, A.N.
TITLE Immunoglobulin kappa light chain variable region gene complex
organization and immunoglobulin genes encoding anti-DNA
autoantibodies in lupus mice
JOURNAL J. Clin. Invest. 82, 852-860 (1988)
MEDLINE 8831394
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
R.Kofler 28-JUL-1988.
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49..105
/note="Ig heavy chain signal peptide"
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BASE COUNT 118 a 120 c 112 g 112 t
 ORIGIN Chromosome 12.

Query Match 79.1%; Score 332.4; DB 13; Length 462;
 Best Local Similarity 88.8%; Pred. No. 2.1e-94;
 Matches 373; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

QY 1 ATGGATGAGAGCTGTATCATCTCTCTTGTGATCAACAGCTACAGTGTCCATCCAG 60
 Db 49 ATGGATGAGAGCTGTATCATCTCTCTTGTGATCAACAGCTACAGTGTCCATCCAG 108
 QY 61 GTCCACTGCAGAGCTGTGGGCTGAGCTGTGAAGCTGGGACTGAGTGAAGCTGTC 120
 Db 109 GTCCACTGCAGAGCTGTGGGCTGAGCTGTGAAGCTGGGACTGAGTGAAGCTGTC 168
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 QY 181 GGACAAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 229 GGACAAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288
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 Db 289 GAGAAAGTTCAGAGGCAAGGCCAATGATGATGATGATGATGATGATGATGATGATGAT 348
 QY 301 CAGCTCAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 349 CAGCTCAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
 QY 361 GAGGATGAGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 408 -----TAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462

RESULT 6
 MUSIGHBX 417 bp mRNA ROD 03-MAY-1985
 LOCUS Mouse Ig active H-chain, C57BL/6 b-NP response from Bl-8, VH-II
 DEFINITION -mRNA.
 ACCESSION J00529
 NID 9195114
 KEYWORDS C-region; V-region; Immunoglobulin heavy chain; variable region
 SOURCE Subgroup VH-II.
 ORGANISM Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorphia; Muridae;
 Murinae; Mus.
 1 (bases 1 to 417)
 Bothwell, A.L.M., Paskind, M., Reth, M., Imanishi-Kari, T., Rajewsky, K.
 and Baltimore, D.
 Heavy chain variable region contribution to the b-NP family of
 antibodies: Somatic mutation evident in a gamma-2a variable region
 Cell 24, 625-637 (1981)
 81234548
 [1] characterized the C57BL/6 response to NP proteins, termed the
 b-NP response because this mouse strain carries the b-1gH
 haplotype.
 Three hybridoma clones were sequenced, two from b-NP hybridomas
 B1-8 and 543 and one from MOPC21 to show the differences between
 b-NP and non-b-NP genes. Seven b-NP-homologous germline genes were
 selected to determine which may be responsible for the b-NP
 response. VH-186-2 seems to be the gene coding for that response
 and is called the b-NP gene. The others are termed b-NP-related

because of their homology with 186-2.
 The BALB/c NP protein response (a-NP, a-1gH haplotype) is reported
 in separate entries.
 Location/Qualifiers

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 /db_xref="taxon:10090"

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CDS
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mat_peptide /note="Ig H-chain V-region from Bl-8 mature peptide"
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BASE COUNT 102 a 107 c 113 g 95 t
 ORIGIN 71 bp upstream of PstI site, chromosome 12.

Query Match 78.7%; Score 330.4; DB 13; Length 417;
 Best Local Similarity 88.3%; Pred. No. 9e-94;
 Matches 371; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 ATGGATGAGAGCTGTATCATCTCTCTTGTGATCAACAGCTACAGTGTCCATCCAG 60
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 Db 61 GTCCACTGCAGAGCTGTGGGCTGAGCTGTGAAGCTGGGACTGAGTGAAGCTGTC 120
 QY 121 TGCAGAGGTATGCTTACACTTACAGCTGATGATGATGATGATGATGATGATGATGAT 180
 Db 121 TGCAGAGGTATGCTTACACTTACAGCTGATGATGATGATGATGATGATGATGATGAT 180
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 Db 181 GGACAAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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 Db 241 GAGAAAGTTCAGAGGCAAGGCCAATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 CAGCTCAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 CAGCTCAGAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 GAGGATGAGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 TAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417

RESULT 7
 AF045487 417 bp mRNA ROD 28-FEB-1998
 LOCUS Mus musculus dc4 anti-poly(dc) monoclonal antibody heavy chain
 DEFINITION variable region, (Igh) mRNA, partial cds.
 ACCESSION AF045487
 NID 92906057
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 417)
 O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
 Anti-DNA antibodies of normal mice immunized with poly(dc) are
 structurally similar to natural autoantibodies

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 417)

AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA

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 /product="anti poly(dC) monoclonal antibody heavy chain"
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J_segment
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BASE COUNT 105 a 103 c 108 g 101 t
 ORIGIN

Query Match 78.3%; Score 328.8; DB 13; Length 417;
 Best Local Similarity 88.1%; Pred. No. 2.9e-93;
 Matches 370; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 1 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTACAGTGTCCACTCCAG 60
 DB 1 ATGGGATGAGCTATATCATCTCTTCTGTATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTAAGCTGGGACTGAGTAAGCTGCC 120
 DB 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTAAGCTGGGACTGAGTAAGCTGCC 120
 QY 121 TGCAGGCTATGCTACCTTACCTTACAGCTACCTGATGCTGGTGAAGAGGCTT 180
 DB 121 TGCAGGCTTCTGGCTACCTTACCTTACAGCTACCTGATGCTGGTGAAGAGGCTT 180
 QY 181 GGACAAGGCTTGTGATGCTGAGAGATGATCTCTGAGAGTAATTAATACTAATAAT 240
 DB 181 GGACAAGGCTTGTGATGCTGAGAGATGATCTCTGAGAGTAATTAATACTAATAAT 240
 QY 241 CAAATTTCAAGGAGGAGCCACATTTGATGATATTCCTCCAGACAGCTTACATG 300
 DB 241 GAGAAAGTTCAGAGCAGCAGCAGCTGATGATGATATTCCTCCAGACAGCTTACATG 300
 QY 301 CAGCTCAGAGCTTGAATGAGAGTCTGCGGTCTACTATTGTGCAAGAGGGGTTAC 360
 DB 301 CAGCTCAGAGCTTGAATGAGAGTCTGCGGTCTACTATTGTGCAAGAGGGGTTAC 360
 QY 361 GAGGATGGAGCTATGCTATGCTACTGGGGTCAAGGACCTGATCAGCGTCTCTCA 420
 DB 361 GAGGATGGAGCTATGCTATGCTACTGGGGTCAAGGACCTGATCAGCGTCTCTCA 420

RESULT 8
 LOCUS MUSIVDJA 429 bp mRNA ROD 25-MAY-1995
 DEFINITION Mus musculus germline immunoglobulin heavy chain variable region,
 diversity region, and joining region, 5' end.
 ACCESSION U35315

NID 9829187
 KEYWORDS diversity region; germline; immunoglobulin heavy chain; joining
 region; variable region.
 SOURCE Mus musculus (strain SJL/J) hyperimmunized spleen mRNA.
 ORGANISM Mus musculus

REFERENCE
 MILLER P.J. and RODRIGUEZ M.
 1 (bases 1 to 429)
 Murinae; Mus.
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;

JOURNAL
 MEDLINE
 COMMENT A monoclonal autoantibody that promotes central nervous system
 remyelination in a model of multiple sclerosis is a natural
 autoantibody encoded by germline immunoglobulin genes
 J. Immunol. 154 (5), 2460-2469 (1995)
 95173452
 On May 24, 1995 this sequence version replaced gi:529401.

FEATURES

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 /organism="Mus musculus"
 /strain="SJL/J"
 /db_xref="taxon:10090"
 /cell_line="SCH94.03"
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 1..>429
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 58..420
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 GYFTSYWMMKORPGQGLEWIMHNPNGSTNNEKFTSKATLTVDKSSSTAYVQF
 SLSLSDSAVYVVRGNLYYAMDYWGQSTVTSVS"

BASE COUNT 108 a 111 c 114 g 96 t
 ORIGIN
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 /note="variable, diversity, and joining regions; putative"
 /product="immunoglobulin heavy chain"

Query Match 78.3%; Score 328.8; DB 13; Length 429;
 Best Local Similarity 86.4%; Pred. No. 2.9e-93;
 Matches 363; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTACAGTGTCCACTCCAG 60
 DB 1 ATGGGATGAGCTGTATCATCTCTTCTGTATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTAAGCTGGGACTGAGTAAGCTGCC 120
 DB 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTGTGTAAGCTGGGACTGAGTAAGCTGCC 120
 QY 121 TGCAGGCTATGCTACCTTACCTTACAGCTACCTGATGCTGGTGAAGAGGCTT 180
 DB 121 TGCAGGCTTCTGGCTACCTTACCTTACAGCTACCTGATGCTGGTGAAGAGGCTT 180
 QY 181 GGACAAGGCTTGTGATGCTGAGAGATGATCTCTGAGAGTAATTAATACTAATAAT 240
 DB 181 GGACAAGGCTTGTGATGCTGAGAGATGATCTCTGAGAGTAATTAATACTAATAAT 240
 QY 241 CAAATTTCAAGGAGGAGCCACATTTGATGATATTCCTCCAGACAGCTTACATG 300
 DB 241 GAGAAAGTTCAGAGCAGCAGCAGCTGATGATGATATTCCTCCAGACAGCTTACATG 300
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 QY 361 GAGGATGGAGCTATGCTATGCTACTGGGGTCAAGGACCTGATCAGCGTCTCTCA 420
 DB 361 TACTACGCTAGTAGGAATTTGACTACTGGGGCAGGACCACTGATCAGAGTCTCTCA 420

RESULT 9
 LOCUS 13384 429 bp DNA PAT 22-JAN-1997
 DEFINITION Sequence 6 from patent US 5591629.
 ACCESSION 13384
 NID 91824175
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 429)
 AUTHORS Rodriguez, M. and Miller, D.J.
 TITLE Monoclonal antibodies which promote central nervous system remyelination
 JOURNAL Patent: US 5591629-A 6 07-JAN-1997;
 FEATURES
 source location/Qualifiers
 1..429
 /organism="unknown"
 BASE COUNT 109 a 111 c 113 g 96 t
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Query Match 77.98; Score 327.2; DB 6; Length 429;
 Best Local Similarity 86.28; Pred. No. 9.2e-93;
 Matches 362; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1 ATGGGATGAGCTGTATCATCTCTCTTGGTATCAACAGCTACAGTCCAG 60
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 QY 61 GTCCACTGCAGCAGCTGGGCTGAGCTGTGAAGCCTGGAGCTCAGTGAAGCTGTC 120
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 QY 121 TGCAGAGGTTATGGCTACACTTTCACACGCTACTGAGTGCAGTGGGTAAAGAGGCT 180
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 QY 301 CAGCTCAGCAGCTGACATCTGAGAGCTCTGCGGTCTACTATTGTGCAAGAGGGCTTAC 360
 Db 301 CAGCTCAGCAGCTGACATCTGAGAGCTCTGCGGTCTACTATTGTGCAAGAGGGCTTAC 360
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 Db 361 TACTACGCTATAGAGACTTTGACTACTGGGCGCAAGCAGCAGCTCAGTCCCTCA 420

RESULT 10
 MMU01972 418 bp mRNA ROD 30-SEP-1993
 LOCUS
 DEFINITION Mus musculus Balb/c anti-CD18 Ig heavy chain variable region mRNA.
 ACCESSION U01972
 NID 9403069
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Mus.
 REFERENCE 1 (bases 1 to 418)
 AUTHORS Hsiao, K., Bajorath, J. and Harris, L.J.
 TITLE Humanization of 60.3, an anti-CD18 antibody
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 418)
 AUTHORS Harris, L.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-1993) Linda J. Harris, Molecular Immunology,
 Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
 Avenue, Seattle, WA 98121 USA
 FEATURES
 source location/Qualifiers
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 /dev_stage="adult"
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 /note="nucleotides 1-25 derived from PCR primer and may not reflect mRNA"
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 1..46
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 47..418
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 58..132
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 58..417
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 133..153
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 154..210
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 211..225
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BASE COUNT 98 a 118 c 110 g 92 t
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Query Match 76.88; Score 322.4; DB 13; Length 418;
 Best Local Similarity 87.18; Pred. No. 3e-91;
 Matches 366; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 ATGGGATGAGCTGTATCATCTCTTGGTATCAACAGCTACAGTCCAG 60
 Db 1 ATGGGATGAGCTGTATCATCTCTTGGTATCAACAGCTACAGTCCAG 60
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 Db 61 GTCCACTGCAGCAGCTGGGCTGAGCTGTGAAGCCTGGGCTCAGTGAAGCTGCC 120
 QY 121 TGCAGAGGTTATGGCTACACTTTCACACGCTACTGAGTGCAGAGAGGCT 180
 Db 121 TGCAGAGGTTATGGCTACACTTTCACACGCTACTGAGTGCAGAGAGGCT 180
 QY 181 GGACAGAGCCTTGTAGTGTGAGAGATGATTCCTTGTGAGAGTAATACATACAT 240

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Db 181 GGAGAGGCGCTGAGTGGATTGGAAGATTGATCTCTCCGATAGTAAGTCACTACAT 240
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Db 241 CAGAGTTCAAGAGGAGCCAGACATTCAGTATGACATTTCTCCAGACAGCCTACATG 300
QY 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTCTACTATTGTGCAAGAGGGGCTTAC 360
Db 301 CAACTCAGACAGCCTGACATCTGAGAGCTCTCGGCTCTACTATTGTGCAAGAGGGGAGCG 360
QY 361 GAGGATGGAGCTATGCTATGACTACTGGGGTCAAGCAGCCTCAGTACCGTCTCTCA 420
Db 361 CTCG---GGTCTTGTGCTATGACTACTGGGGTCAAGCAGCCTCAGTACCGTCTCTCA 417

RESULT 11
AF045499 420 bp mRNA ROD 28-FEB-1998
LOCUS Mus musculus 5E3 monoclonal antibody heavy chain variable region,
DEFINITION (IGH) mRNA, partial cds.
ACCESSION AF045499
NID g2906081
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 420)
AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Anti-DNA antibodies of normal mice immunized with poly(DC) are structurally similar to natural autoantibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 420)
AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA

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58..351
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D_segment /gene="IGH"
376..>420
J_segment /gene="IGH"
BASE COUNT 97 a 104 c 121 g 98 t

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Best Local Similarity 85.0%; Pred. No. 3e-90;
Matches 357; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGGAGTGGAGCTGATCATCTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60

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Db 1 ATGGAGTGGAGCTGATCATCTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
QY 61 GTCCAGTGCAGAGCCTGGGGCTGAGCTGTGAAGCTGGGACTTGAAGTGAAGTGC 120
Db 61 GTCCAGTGCAGAGCCTGGGGCTGAGCTGTGAAGCTGGGACTTGAAGTGAAGTGC 120
QY 121 TGCAGAGTTATGCTACCTTCACCTTCACCACTGATGATGCACTGGGTGAAGAGCCT 180
Db 121 TGCAGAGTTATGCTACCTTCACCTTCACCACTGATGATGCACTGGGTGAAGAGCCT 180
QY 181 GGACAGGCGCTTGATGGATGGAGAGATTGATCTCTGAGAGTAATTAATACTACAT 240
Db 181 GGACAGGCGCTTGATGGATGGAGAGATTGATCTCTGAGAGTAATTAATACTACAT 240
QY 241 CAAATTCAGAGGAGCCAGACATTCAGTATGACATTTCTCCAGACAGCCTACATG 300
Db 241 CAGAGTTCAAGAGGAGCCAGACATTCAGTATGACATTTCTCCAGACAGCCTACATG 300
QY 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTCTACTATTGTGCAAGAGGGGCTTAC 360
Db 301 CAGCTCAGACAGCCTGACATCTGAGAGCTCTCGGCTCTACTATTGTGCAAGAGTACCTAT 360
QY 361 GAGGATGGAGCTATGCTATGACTACTGGGGTCAAGCAGCCTCAGTACCGTCTCTCA 420
Db 361 GATTCAGAGGCGGCGCTGGTTGCTTACTGAGGCGCAAGGAGCTGTGACATGTCTCTCA 420

RESULT 12
MUSIGHYXA 1069 bp DNA ROD 29-SEP-1993
LOCUS Mouse (hybridoma 3A112) Immunoglobulin heavy chain variable region.
DEFINITION I09566
ACCESSION g196111
NID
KEYWORDS heavy chain; immunoglobulin; rearranged variable region; variable region.
SOURCE Mus musculus (strain C57BL/6J, sub-species domesticus) DNA.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1069)
AUTHORS Rothenfluh,H.S., Taylor,L., Bothwell,A.L., Both,G.W. and Steele,E.J.
TITLE Somatic hypermutation in 5' flanking regions of heavy chain antibody variable regions
JOURNAL Eur. J. Immunol. 23 (9), 2152-2159 (1993)
MEDLINE 93380482
FEATURES
source 1..1069
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/db_xref="taxon:10090"
promoter 461..468
TATA_signal 491..494
mRNA 520..1069
BASE COUNT 272 a 236 c 242 g 313 t 6 others

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Query Match 75.5%; Score 317.2; DB 13; Length 1069;
Best Local Similarity 86.5%; Pred. No. 1.5e-89;
Matches 346; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Db 670 CATCCACTTTCCTTCTCTCCACAGGATGCCATCCAGGTCCCAACTGCAGCAGCTGG 729
QY 81 GAGCTAGCTGTGAAGCCTGGGACTCAGTGAAGCTCTCCGCAAGGGTATATGCTCAAC 140
Db 730 GAGCTAGCTGTGAAGCCTGGGACTCAGTGAAGCTCTCCGCAAGGGTATATGCTCAAC 140
QY 141 CTTACAGCTACTGATGAGCTGGGTGAAGCAGAGGCTTGAGACAGGCTTGAAGTGAAT 200
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Db	790	CTCCACAGCTACTTGATGCATCGGGTGAAGCAGAGCGCTGGCCAAAGCCTTGATGGAT	849
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Db	850	TGGAGGATTTGATCTCTCTGATGGTATTTCTAATCAATCAAAAGTTCAAGACCAAGC	909
Qy	261	CACATTGACTGTAGACATTTCTCTCCAGCAGCAGCTCATGTCAGTCAGACGCTGATC	320
Db	910	CACACTGACTGTAGACAAACCTCTCCAGCAGAGCTTACATGCAAGCTCAGACGCTGATC	969
Qy	321	TGAGGACTCTGCGGCTCTACTATTGTGCAAGAGGGGTTTACAGCGGATGGACTTACTAT	380
Db	970	TGAAGAACTCTGCGGCTCTATTATTGTGCAAGANNNNNNATATGGTTTCCTTACTCTGCTAT	1029
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RESULT		13				27-JUN-1995
A27941						
LOCUS	A27941		501 bp	DNA	PAT	
DEFINITION	Coding region for humanised antibody.					
ACCESSION	A27941					
NID	g1248529					
KEYWORDS	.					
SOURCE	unidentified.					
ORGANISM	unidentified.					
REFERENCE	unclassified.					
AUTHORS	1 (bases 1 to 501)					
TITLE	HUMANIZED AND CHIMERIC MONOCLONAL ANTIBODIES					
JOURNAL	Patent; WO 9215683-A 31.17-SEP-1992;					
FEATURES	Location/Qualifiers					

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BASE COUNT      127 a      146 c      124 g      104 t
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Best Local Similarity	84.3%	Pred. No. 1e-88		
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			Gaps	0

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OY	61	GTCACACTGCACAGCCTGGGGCTGAGCTTGTGAAGCCGAGCACTTCAATGAACTGCC	120
Db	91	GTCACGCTGCACAACACTGGGGCTAAGCTGGTGAAGCCCTGGGGCTTCAATGAAGTGGC	150
OY	121	TGCAGGGTTATGGCTACACCTTCAACCAAGTACTGGATGCACTGGGTGAAGCAGGCGCT	180
Db	151	TGCAGGGTTCGGGTACACCTTCAACCAAGCCTGGATGCACTGGGTGAAGGAGGGCT	210
OY	181	GGACAAGCCTTGAATGATCGAGAGAGATGTGCTTGTGAGAGTAATACTACTACAT	240
Db	211	GGACAAGCCTTGAATGATCGAGAGAGTATATCCACGAACAGCGCGTACTACTACAT	270
OY	241	CAAAATTCAGAGGCGCAAGCCACATTTGACTGTAGACATTTCTCCAGACAGCCTCATG	300

[illegible]

RESULT	14								
LOCUS	126277								
DEFINITION	Sequence 23 from patent US 5558864.						PAT	30-SEP-1996	
ACCESSION	126277								
NID	91606147								
KEYWORDS	.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 501)								
TITLE	Bendig/M.M., Kettileborough/C.A. and Saldanha,J. Humanized and chimeric anti-epidermal growth factor receptor monoclonal antibodies Patent: US 5558864-A 23 24-SEP-1996;								
JOURNAL	Location/Qualifiers								
FEATURES	1..501								
source	/organism="unknown"								
BASE COUNT	127 a 146 c 124 g 104 t								
ORIGIN									

Query Match	74.9%	Score 314.4	DB 6	Length 501
Best Local Similarity	84.3%	Pred. No. 1e-88		
Matches 354	Conservative	0	Mismatches 60	Indels 0
				Gaps 0
QY	1	ATGGGATGAGAGCTGTATCATCTCTCTTCTTGGTATCAACAGCTACAAAGTGTCCACTCCAG	60	
Db	31	ATGGGTTGGAGCTATATCATCTCTTTTGGTAGCAACAGCTACAGATGTCCACTCCAG	90	
QY	61	GTCACATGACAGCAGCCCTGGGGCTGAGCTTGTGAAGCCTGGAGCTTCACTGAGCTGCC	120	
Db	91	GTCGCACTGCACAACTGGGGCTGACTGGGAGACCTGGGGCTTCACTGAGGTTGTCC	150	
QY	121	TGCAGGGGTTATGGCTACACCTTCACACGCTTCTGGATGACATGGGTGGAAGAGGGCT	180	
Db	151	TGCAGAGCTTCCGGGTACACCTTCACACGCTGATGACATGGGTGGAAGAGGGCT	210	
QY	181	GGACAAAGGCTTGTAGTGTATGGAGAGATTTGCTTGTGAGATTAATCTAATACAT	240	
Db	211	GGACAAAGGCTTGTAGTGTATGGAGAGATTTATCCAGCAAGCGCGTACTAATACAT	270	
QY	241	CAAAAATTCAGGGGCAAGGCCACATTTGACTGTAGACATTTCTCCAGCAGACCTTACATG	300	
Db	271	GGAATTCAGAGCAAGGCGCACACTGACTGTAGCAAAATCTCCAGCAGACCTTACATG	330	
QY	301	CAGCTCAGAGCCTACATCTGAGAGACCTGGGGCTACTATTGGCAAGGGGGTAC	360	
Db	331	CAGCTCAGAGCCTACATCTGAGAGACCTGGGGCTATTATGTGCCAGTGGGACTAT	390	
QY	361	GACGATGGAGATATGCTATTGACTACTGAGGGGTCAAGGACACTCAGTACCGCTCTCTCA	420	
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RESULT 15

MUSIGHPG MUSIGHPG 471 bp mRNA ROD 15-MAR-1990

LOCUS M27788

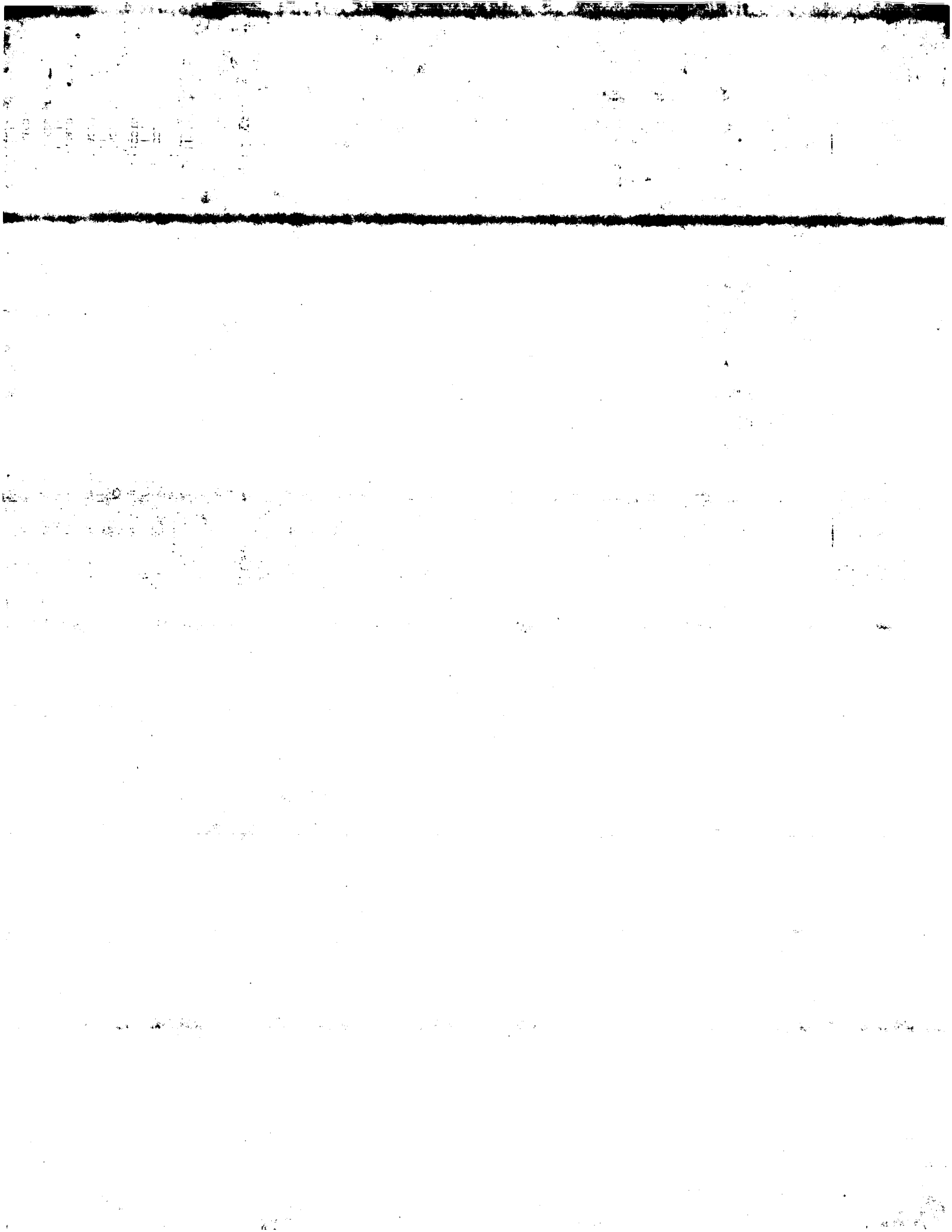
DEFINITION Mouse Ig active mu-chain mRNA V-D-J2-C region, clone 18C10.

ACCESSION

NTD g195851

KEYWORDS C-region; D-region; J-region; V-region; Immunoglobulin heavy chain;
SOURCE Immunoglobulin mu-chain; processed gene.
ORGANISM Mouse spleen, cDNA to mRNA, clone 18C10.
Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kaartinen, M., Rocca-Serra, J. and Maekela, O.
TITLE Combinatorial association of V genes: One V-H gene codes for three
non-cross-reactive monoclonal antibodies each specific for a
different antigen (phoxalone, NP or GAT)
JOURNAL Mol. Immunol. 25, 859-865 (1988)
MEDLINE 89096973
FEATURES
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BASE COUNT 113 a 126 c 127 g 101 t 4 others
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Best Local Similarity 86.4%; Pred. No. 3.2e-88;
Matches 363; Conservative 0; Mismatches 42; Indels 15; Gaps 1;
QY 1 ATGGGATGAGCTGATCATCCTCTTCTGGATCAACAGCTACAGTGTCCACTCCAG 60
DB 49 ATGGGATGAGCTGATCATCCTCTTCTGGATCAACAGCTACAGTGTCCACTCCAG 108
QY 61 GTCCAATGCAAGCCTGGGGCTGAGCTGTGAAGCCTGGACTTCAGTGAAGCTGTCC 120
DB 109 GTCCAATGCAAGCCTGGGGCTGAGCTGTGAAGCCTGGACTTCAGTGAAGCTGTCC 168
QY 121 TGAAGGGTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 180
DB 169 TGAAGGGTATGCTACACCTTACACCTGATGATGATGATGATGATGATGATGATGAT 228
QY 181 GGACAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 229 GGACAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288
QY 241 CAAAATTCAGAGGCAAGCCATTTGACTGATGATGATGATGATGATGATGATGATGAT 300
DB 289 GAGAAAGTCAAGAGCCAGCCACTGATGATGATGATGATGATGATGATGATGATGAT 348
QY 301 CAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 349 CAGCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 408
QY 361 GACGATGAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 409 GCCGG-----GGACTACTGGGGCCAGGACACACTCTTCACAGTCTCTCA 453

Search completed: May 11, 1999, 12:00:29
Job time: 1476 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:10 ; Search time 479.58 Seconds

(Without alignments)
1335.915 Million cell updates/sec

Title: US-08-700-737-14

Perfect score: 420
Sequence: 1 ATGGGATGAGCTGTATCAT.....CTTCAGTCACCGTCTCTCA 420

Scoring table: IDENTITY_NUC

Searched: 2002476 segs, 762712212 residues

Database :

EST:*

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41:	em_est19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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2	215.6	51.3	294	28	A1007196	ua73g04.r

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	5	147.8	35.2	279	17	AA300571	EA300571 EST13661
	6	140.4	33.4	431	25	AA710970	AA710970 vt93h09.r
	7	136.8	32.6	287	11	T27609	T27609 EST101034.H
	8	136	32.4	336	29	AA987559	AA987559 cr83g01.s
	9	135.2	32.2	291	18	AA377074	AA377074 EST89603
	10	134	31.9	379	21	AA291381	AA291381 zt44g02.r
	11	132.2	31.5	823	16	AA170256	AA170256 ms87g10.r
	12	127.8	30.4	238	11	T29670	T29670 EST89669.Ho
	13	125.8	30.0	265	18	AA377128	AA377128 EST89660
	14	116	27.6	432	31	A1286604	A1286604 q047a10.x
	15	113.6	27.0	372	25	AA581192	AA581192 nd38d11.x
c	16	104.4	24.9	109	11	T28938	T28938 EST61186.Ho
	17	102.4	24.4	198	19	AA383972	AA383972 EST97425
c	18	97.8	23.3	378	26	AA740786	AA740786 cb32e11.s
	19	97.4	23.2	385	11	R86288	R86288 yp12e09.r1
	20	95.2	22.7	630	27	AA895088	AA895088 vy32h01.r
	21	94.2	22.4	330	14	SSC1D10	F14516 S.scrofa.mr
	22	91.8	21.9	238	21	AA505044	AA505044 aa63g01.r
	23	89.2	21.2	116	30	A1116236	A1116236 uc18e08.r
	24	89	21.2	419	12	H73816	H73816 vs11b01.r1
c	25	87.4	20.8	474	31	A1147237	A1147237 qb36f02.x
	26	83.4	19.9	432	21	AA544384	AA544384 vk3f04.r
c	27	80.4	19.1	488	29	AA948436	AA948436 on67a01.s
	28	80	19.0	304	17	AA300945	AA300945 EST13823
	29	79.2	18.9	364	16	AA098196	AA098196 mn86h06.r
	30	78	18.6	430	11	R72787	R72787 yj91h09.r1
	31	75.2	17.9	403	26	AA715258	AA715258 nv35a08.r
	32	74.8	17.8	239	11	T27727	T27727 EST13874.Ho
	33	73.4	17.5	597	20	AA472093	AA472093 v10a05.r
	34	72.6	17.3	415	22	AA575218	AA575218 v10a01.r
	35	72.2	17.2	297	11	T27868	T27868 EST18962.Ho
	36	71.8	17.1	266	24	AA402547	AA402547 zu47h07.r
c	37	71	16.9	247	27	AA897116	AA897116 am08b07.s
	38	70.8	16.9	485	29	AA988730	AA988730 or79h12.s
c	39	70.4	16.8	303	11	R83139	R83139 yp11g03.r1
	40	66.4	15.8	258	18	AA360195	AA360195 EST69374
	41	65.8	15.7	478	11	H43753	H43753 yp21g01.r1
	42	65.2	15.5	278	19	AA381086	AA381086 EST94138
	43	64.6	15.4	273	17	AA300982	AA300982 EST13889
	44	62	14.8	280	17	AA326955	AA326955 EST30467
	45	61	14.5	426	30	A1124611	A1124611 am59d10.x

ALIGNMENTS

RESULT	1	EST	08-OCT-1998
LOCUS	A1180569	uc70f09.r1	Soares mouse mammary gland NbmMG Mus musculus CDNA clone
DEFINITION	1431017 5' similar to gb:MI2376 Mouse Immunoglobulin H-chain V-region pseudogene (HUMAN); gb:MI2376 Mouse Immunoglobulin H-chain V-region pseudogene mRNA, complete (MUSE);, mRNA sequence.		
ACCESSION	A1180569		
NID	93731207		
KEYWORDS	EST		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 310)		
	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project		

	RESULT	3
	AA569186	
	LOCUS	
	DEFINITION	mRNA sequence.
	ACCESSION	J2342240
	NID	EST.
	KEYWORDS	human.
	SOURCE	Homo sapiens Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 387) NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap/ National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
	JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/WLND at: www.bio.linnl.gov/dbrip/image/Image.html
	FEATURES	Insert Length: 1722 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amershams High quality sequence stop: 284.
	SOURCE	Location/Qualifiers 1..387 organism="Homo sapiens" note="Vector: pAMP10; mRNA made from lposarcoma, cDNA made by oligo-dt priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383." db_xref="taxon:9606" clone_image=1061683 clone_1lb="NCI_CGAP_L1P2" tisue_type="liposarcoma" lab_host="DH10B"
BASE COUNT	MRNA	89 A 95 C 118 G 85 T
ORIGIN		<1..>387

	Query Match	46.8%	Score 196.4	DB 52	Length 387
	Best Local Similarity	72.6%	Pred. No. 5.7e-52		
	Matches 254	Conservative 0	Mismatches 96	Indels 0	Gaps 0
OY	1 ATGGAGATGAGCTGTATCATCTCTCTTGGTATCAACAGCTACAGTGTCCACTCCAG	60			
Db	38 ATGGAGCTGACCTGGAGGGCTTCTGCTGTGCTGGCTGTAGCCAGTGTCTACTCCAG	97			
OY	61 GTCCACATGCAAGCACTGGGGCTAGGCTGTGAAGCCGTGAGTGAAGTGTCC	120			
Db	98 GTCCACATGTGTCTGATCTGGGGCTAGGCTGAAGAACCTGGGGCTCTGTGAAGTTC	157			
OY	121 TCCAAAGGTTATGCTACACCTTCACCAAGCTACTGGATGCTGGGTGAAGCAGGGCT	180			
Db	158 TGTAAAGCATCTGGGATTCACCTCTCAACCAACTGCCATATGCACTGGGTGGCAGAGCCCT	217			
OY	181 GGACAGAGCCTTGAATGTGATCGAAGAGATGTATCTCTTGAGAGATTAACATACTAACAT	240			
Db	218 GGGCAGAGGCTTGATGTGGGTGGGAATGATCAATTAGTGAATGTTATTAATAGTAAACGA	277			
OY	241 CAAAAATTCAGAGGCAAGCCACATTGACTGTAGACATTTCTCCAGCACAGCCTTACATG	300			

Dd	278	CAGAAGTTCGAGGGCAGACGTCAATCATGCACAGGACACTCCACAGCACAGCTATTATG	337
OY	301	CAGTCACAGCGCTTGACATCTGAGGACCTCTGCCGTCTACTAATTGTGA	350
Dd	338	GAGCTTAGACAGCTGAGATCTGAGGACACAGGCCCTCTATTACTGTGGC	387
<hr/>			
RESULT 4 LOCUS AI201426/c			
DEFINITION gsf3c06.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:1943722 3'			
FEATURES similar to db:M8512 IG HEAVY CHAIN PRECURSOR V-I REGION (HMAN); contains Alu repetitive element; mRNA sequence.			
ACCESSION AI201426			
NID g3754032			
KEYWORDS EST .			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;			
Primates; Catarrhini; Homnidae; Homo.			
REFERENCE 1 (bases 1 to 461)			
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
<hr/>			
Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov			
unknown library type			
Insert Length: 608 Std Error: 0.00			
Seq primer: -40UP from GlDco.			
Location/Qualifiers			
FEATURES	1..461		
source	/organism="Homo sapiens"		
	/note="Organ: prostate; Vector: pT7TD-Pac (Pharmacia)		
	with a modified polylinker; Plasmid DNA from the		
	normalized library NCI_CGAP_Pt2 was prepared, and ss		
	circles were made in vitro. Following HAP purification,		
	this DNA was used as tracer in a subtractive hybridization		
	reaction. The driver was PCR-amplified cDNAs from a pool		
	of 5,000 clones made from the same library (clonids		
	985608-986759, 1101192-1101959, and 121928-1220615).		
	. Subtraction by Bento Soares and W. Fatima Bonaldo."		
	/db_xref="taxon:9606"		
	/clone_image="IMAGE:1943722"		
	/clone_lib="NCI_CGAP_Pt28"		
	/sex="male"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
BASE COUNT	93 a 132 c 106 g 130 t		
ORIGIN			
<hr/>			
Query Match 43.7%; Score 183.6; DB 31; Length 461; Best Local Similarity 73.6%; Pred.No. 6,6e-48; Matches 234; Conservative 0; Mismatches 84; Indels 0; Gaps 0;			
OY	35	CACAAGCTACAAAGTGTCCACTTCCCAGTCCAATGTCAGACACCCTGGGCTGAGCTTTGA	94
Dd	461	CACCAAGCTACAGGTGCCCCACTGCCAGGTGAGCTGTCAGTCTGGGGCTGAGTGAGA	402
OY	95	AAGCCGGGACCTTCAGTGAAGCTGTCCTCCAGAGGGTAAGCTACACCTTCACACACTACT	154
Dd	401	AGCCGGGGGCTCATGTAAGGTCCTCCCAAAGGCTTCGGATACTTCACCCGACTACT	342
OY	155	GGATGACATGGGTGAGACAGAGCCTGAGCAAGGCTTGATGATGATGATGATGATC	214
Dd	341	ATATGCAATGGGTGGAGAGGCCCCCTGGACAAAGACTTGGGTGATGGAGAGGATCAACC	282
OY	215	CTTGAGAGTAATCTACTACAAATTCAAAATTCAGGGCCAGGCCACTTACTGTG	274

Db	281	CTACAGCGTGGGCAACAACATCATCAGAGAAGTTTCAGGGGCAGAGTCACATCAGCAAGGG	222
Oy	275	AAATTTCCTCCAGCACACGCTTACTGACGTCAAGCACCCTGACATCTGAGAGACTCTGCCG	334
Db	221	ACAGCTCATCATGAGACAGACCCCTACAGGAGGTGAGCAGCAGCTTGAGATCTGAGACACGGCCA	162
Oy	335	TCTACTATTGTGCAAGAG	352
Db	161	CCTATTACTGTGCGAGAG	144
RESULT	5		
LOCUS	AA300571		
DEFINITION	ES113661 Testis tumor Homo sapiens cDNA 5' end similar to similar to Immunoglobulin mu heavy chain, VDJC regions (GB:M19512), mRNA sequence.	EST	18-APR-1997
ACCESSION	AA300571		
NID	q1953132		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 279)		
REFERENCE	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullmer,R.A., White,C.J., Lee,N.H., Kitznes,E.F., Weinstock,K.G., Gocayne,J.D., Bult,C., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgenard,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pellierino,S.M, Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Welden,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.R., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,U., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Pannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C. Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl.), 3-174 (1995) 96026280		
JOURNAL	Other-ESTs: THCI66571		
MEDLINE	Contact: Kerlavage, AR		
COMMENT	Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel.: 3016699056 Fax: 3016699423 Email: akertavel@tigr.org Information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/ngl/ngl.html) Seq primer: M13 Reverse. Location/Qualifiers 1..279 /organism="Homo sapiens" /note="Organ: testis; Vector: pBluescript SK-; Site_1: ECORI: Site_2: XhoI" /db_xref="ATCC (inhost):192212" /db_xref="taxon:9606" /clone_id="Testis tumor" /sex="male" /dev_stage="adult" <1..>279 63 a 74 c 85 g 56 t 1 others		
BASE COUNT	63 a 74 c 85 g 56 t 1 others		
ORIGIN			

Query Match	35.2%	Score 147.8;	DB 17;	Length 279;
Best Local Similarity	74.6%;	Pred. No. 1.2e-36;		
Matches 185;	Conservative	0;	Mismatches 63;	Indels 0;
			Gaps	0;
Qy	1	ATGGGATGAGGTGTATATCCCTCTTCTTGTGATCAACAGCTACAAAGTGTCCACTCCAG	60	
Db	32	ATGGACTGTGACCTGGAGGATCCTCTTCTTGTGTGGGAGCAGCACGACGAGGCCACTCCAG	91	
Qy	61	GTCCAACTGCAGCAGCCCTGGGGCTGAGCTTGTGAACCTGGGACCTTCAATGAAGCTGTCC	120	
Db	92	GTGCAGCTGTGTCACTCTGGGGCTGAGGTGAAGAAGCCTGGGGGCTCATGTGAAGTCTCC	151	
Qy	121	TGCAAGGGTATGCTATCAACCTTACCAAGCTACTGATGCACTGGGTGAAGCAGAGCCT	180	
Db	152	TGCAAGGGCTTCGTGATTAACCTTCAACCGGCTACTATATGCACTGGGTGGCAGAGGCCCT	211	
Qy	181	GGACAGAGCGCTTGATGTCGAGAGAGATGTATCCCTTGAGAGTAATCTAATACATAAT	240	
Db	212	GGACAAAGGCTTNACTGATGGATGGATGATCAACCTTAAAGTGTGTGGCACAACAATATGCA	271	
Qy	241	CAAAAATT 248		
Db	272	CAGAGTT 279		

RESULT	6
AA710970	
LOCUS	AA710970
DEFINITION	AA710970 431 bp mRNA EST 24-DEC-1997 v93h09.71 Soares mouse mammary gland NBXMG Mus musculus cDNA clone 118753 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HMANA); gb:x70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE); , mRNA sequence.
ACCESSION	AA710970
NID	92720888
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus. Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 431) Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcoe,W., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
AUTHORS	The WashU-HMHI Mouse EST Project Unpublished (1996)
TITLE	Contact: Marra M/Mouse Est Project
JOURNAL	WashU-HMHI Mouse EST Project
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mousest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. MGI:636601 Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 198. Location/Qualifiers 1..431 /organism="Mus musculus" /strain="C57BL/6J" /note="Organ: mammary gland, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAGATCTGAGAGCGGCGCCGCAAGCTTTTTTTTTTTTTTTTTTTT T 3)]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector.
FEATURES	SOURCE

Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback,
Weidman, T.F., Wilby, R., Winkler, D.P., Zuo, L., Canada, V.A.

Journal
published (1951)
Comment
Contact: Robert Strausberg, Ph.D.
2000 University Avenue
Berkeley, CA 94704-1500
USA
Tel: 415 849 2200
Fax: 415 849 2201
E-mail: rs@uclink.berkeley.edu


```

Db      255 CAGAAATTTCGGGGAGAGATCACTCCCTGACCGAGACA 291

RESULT 10
LOCUS   AA291381          379 bp      mRNA          EST          08-AUG-1997
DEFINITION
5' zt44902.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone 725234
(HUMAN); mRNA sequence.
ACCESSION
AA291381
NID     91939359
KEYWORDS
SOURCE  human.
ORGANISM
Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

REFERENCE
AUTHORS 1 (bases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifein,L., Rohlfing,T., Tan,F., Trevasakis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
Washu-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1576 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
1. 379
/organism="Homo sapiens"
/Note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAGAGGAGGCGCGCGGTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_id="725234"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1. >379

BASE COUNT      85 a      82 c      121 g      91 t
ORIGIN
mRNA
BASE COUNT      85 a      82 c      121 g      91 t
ORIGIN

Query Match      31.9%; Score 134; DB 21; Length 379;
Best Local Similarity 66.1%; Pred. No. 2.9e-32;
Matches 209; Conservative 0; Mismatches 105; Indels 2; Gaps 1;

37 ACACCTACAGATGTCACCTCCAGTCCCACTGCAGACGCTGGGCTGAGCTGTGAG 96
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 ACACCTACAGATGTCACCTCCAGTCCCACTGCAGACGCTGGGCTGAGCTGTGAG 72
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 CCTGGAGCTTCACTGAGAGCTCTCTGCAAGGTTATGGCTACACCTACCACTACTGG 156
| ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 73 CTGGGGCC--CAGTGAAGGCTCTCTGTAAGACCTCTGTTACACTTTGGCATTTCGT 130
|| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||
QY 157 ATGCACTGGGTGAAGCAGAGGCTTGAGACAGGCTTGATGATCGAGAGATTGATCT 216
|| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||

```

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Db      131 ATCACTGGGTGGCGGAGGCCCCCTGACAAAGGCTTGATGATGGATGATCAGCCTT 190

QY 217 TCTGAGAGTAATACTACTACATAAATCAAAATTCAGAGGAGCCACATGACTGTAGAC 276
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 191 TACATGTGTAAGACAAACTTTGCAGGAGATTTCAGACAGATGACTGTGACACATGAC 250
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
QY 277 ATTTCCTGCAGACAGGCTTACATGACCTGACAGCCTGACATCTGAGGACTGTGCGTC 336
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 251 ACATCCAGATACAGAGCTTACATGAGACTGAGGAACCTGATGATGACGACAGGCCATA 310
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
QY 337 TACTATTGTGCAAGAG 352
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 311 TATTACTGTGCGAGAG 326
| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |

RESULT 11
LOCUS   AA170256          823 bp      mRNA          EST          16-FEB-1997
DEFINITION
ms87910.r1 Soares mouse 3NBMS Mus musculus cDNA clone 618594 5'
similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN);
gb:Y00821 Mouse mRNA fragment for immunoglobulin mu encoding the
C-terminus (MOUSE); mRNA sequence.
ACCESSION
AA170256
NID     91746794
KEYWORDS
SOURCE  house mouse.
ORGANISM
Mus musculus
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE
AUTHORS 1 (bases 1 to 823)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacey,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The Washu-HMI Mouse EST Project
Unpublished (1996)

TITLE
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestevatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:379418
Putative full length read
vector to vector length is 867
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 492.
Location/Qualifiers
1. 823
/organism="Mus musculus"
/strain="C57BL/6J"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTGAGAGGAGGCGCGCGGTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"
/clone_id="618594"
/clone_lib="Soares mouse 3NBMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"

```


Journal Comment

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies Inc., David Krizman,
Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNLT at:
www-Dio.lim.gov/bdnp/image/image.html

Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.

FEATURES	Location/Qualifiers
source	1. .372

BASE COUNT	81 a	83 c	122 g	86 t
ORIGIN				

Query Match	27.0%;	Score 113.6;	DB 25;	Length 372;
Best Local Similarity	57.7%;	Pred. No. 8.1e-26;		
Matches 203; Conservative	0;	Mismatches 149;	Indels 0;	Gaps 0;

Oy	1	ATGGATATGAGCTGATATATCTCTCTTCTGGTATACAAAGCTACAAAGTGCATCTCCG	60
Db	21	ATGAGATTGGGGCTGAGCTGGCTTTTCTTTGTGGCTATTTTAAAGGTGTCACTGTGAG	80
Oy	61	GTCCAATGCACAGACCTGGGGCTTGAGCTTGTGAACCTGGGACTTAGTGAAGCTGCC	120
Db	81	GTCCAGCTGTTTGGATCTCTGGGGGAGGCATGTGTACAGGCTGGGGGGTCCCTGAGACTCTCC	140
Oy	121	TGCAGGGTTTATGGCTTACACCTTACCAACGATCTGAGATGCACCTGGGTGAAGACAGAGGCT	180
Db	141	TGTGAGGCTCTGTGATTTACCTTTAGCAGGCATGCAAGACTGGGTCCGCGACAGGTCCA	200
Oy	181	GGACAGGCCCTTGAATGAGTATGGAGAGATTGATTCCTTGTAGAGTAAATTAATACTACTAAT	240
Db	201	GGGAGGGGGCTGGAATGGGTCTCATCTTATAGTGTGTGTGTATACACATACTATACGA	260
Oy	241	CAAAATTCAGAGGGCGAAGGCACATTTGACTGTATAGACATTTCTCCAGACAGCCTATACG	300
Db	261	GACTCCGTGAAGGGCGGTTACACATCTCCAGAGACAAATTCAGAAACACGCTGTATATG	320
Oy	301	CAGCTCAGACAGCTTACATCTGAGAGATCTCTCGGCTTACTTGTGTGCAAGG	352
Db	321	CAAGTAACACCTGTAGAGCCGAGAGACAGGGCCGTATATTACTGTGGGAAG	372

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:03:26 ; Search time 88.51 Seconds

(without alignments)
892.725 Million cell updates/sec

Title: US-08-700-737-14

Perfect score: 420
Sequence: 1 AUGGATGAGAGCTGATCAT.....CCTCACTACCGCTCTCTCA 420

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database: N_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	420	100.0	420	1	V20078	DNA encoding murin
2	416.4	99.1	494	1	V20085	Consensus DNA sequ
3	406.2	96.7	428	1	V20089	DNA sequence of mu
4	359.2	85.5	540	1	V20076	DNA encoding the h
5	335.8	80.0	1582	1	O94037	Mab 55.1 heavy cha
6	330.4	78.7	458	1	Q15164	VH186 region of an
7	327.2	77.9	429	1	T05312	MAB SCH94.03 heavy
8	314.4	74.9	501	1	Q28739	CDNA of VH425 anti
9	308.4	73.4	499	1	T38509	Heavy chain coding
10	298	71.0	433	1	T36303	Anti-hepatitis B h
11	298	71.0	420	1	T36304	Anti-hepatitis B h
12	298	71.0	420	1	V18553	Human anti-hepatit
13	298	71.0	433	1	V18554	Human anti-hepatit
14	298	71.0	433	1	V03866	Human anti-hepatit
15	298	71.0	420	1	V03836	Human anti-hepatit
16	298	71.0	420	1	V18589	Human anti-hepatit
17	298	71.0	433	1	V18590	Human anti-hepatit
18	296.4	70.6	420	1	N70967	Sequence of the an
19	296.4	70.6	420	1	N70968	Sequence of the an
20	296.4	70.6	420	1	T51039	Chimeric anti-hepa
21	296.4	70.6	433	1	T70857	Mouse-human chimae
22	296.4	70.6	420	1	T70858	Mouse-human chimae
23	294.4	70.1	3058	1	T77137	Single chain anti
24	293.6	69.9	357	1	T04016	Anti-EGFR antibody
25	293	69.8	357	1	T43805	Anti-DNA antibody
26	292	69.5	477	1	Q12057	Sequence encoding
27	292	69.5	477	1	Q12013	Sequence encoding
28	290.8	69.2	1284	1	T77139	Single chain anti
29	287.6	68.5	440	1	V22074	DNA encoding the h
30	287.2	68.4	471	1	T43438	Mab Co-1 heavy cha
31	283	67.4	416	1	T85854	Anti-HMG MAB CTMO
32	282.4	67.2	471	1	Q08607	Co-1 Heavy Chain V
33	282.4	67.2	357	1	T58252	Lead binding Mab 8
34	281.8	67.1	357	1	T04014	Anti-EGFR antibody
35	281.4	67.0	416	1	Q38877	CTMO1 VH cDNA. Ant
36	280.6	66.8	1553	1	Q79930	Anti-tobacco mosai
37	280.2	66.7	858	1	Q64817	PRAS11 between H1
38	280.2	66.7	858	1	Q70658	SCFV PRAS107 and p
39	280.2	66.7	1356	1	Q70659	SCFV PRAS108 and p
40	280.2	66.7	1257	1	Q70661	SCFV PRAS110 and p
41	280.2	66.7	1259	1	Q70662	SCFV-BRNase fusio
42	280.2	66.7	1648	1	Q70665	SCFV-DNaseI fusion
43	279.2	66.5	411	1	V12263	Monoclonal antibod

ALIGNMENTS

RESULT	ID	Sequence	Score	DB	Length	Matches	Mismatches	Indels	Gaps
1	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
2	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
3	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
4	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
5	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
6	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
7	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
8	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
9	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
10	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
11	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
12	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
13	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
14	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
15	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
16	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
17	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
18	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
19	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
20	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
21	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
22	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
23	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
24	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
25	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
26	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
27	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
28	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
29	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
30	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
31	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
32	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
33	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
34	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
35	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
36	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
37	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
38	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
39	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
40	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
41	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
42	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0
43	V20078	standard; DNA; 420 BP.	100.0%	1	420	420	0	0	0

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QY 241 CAAATTCAGAGGCAAGCCATTCAGTGTAGACATTTCTCAGACACCTACATG 300
|
|
|
Db 241 CAAATTCAGAGGCAAGCCATTCAGTGTAGACATTTCTCAGACACCTACATG 300
|
|
|
QY 301 CAGCTCAGACGCTGACATCTGAGACTCTCGGCTCTACTTGTGTGCAAGGGGGTTAC 360
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Db 301 CAGCTCAGACGCTGACATCTGAGACTCTCGGCTCTACTTGTGTGCAAGGGGGTTAC 360
|
|
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QY 361 GAGGATGGGACTATGCTATGACTAGTGGGCTCAAGGACCTCAGTCACCGTCTCCCA 420
|
|
|
Db 361 GAGGATGGGACTATGCTATGACTAGTGGGCTCAAGGACCTCAGTCACCGTCTCCCA 420
|
|
|
RESULT 2
V20085
ID V20085 standard; DNA; 494 BP.
AC V20085;
DT 14-JUL-1998 (first entry)
DE Consensus DNA sequence of the murine variable heavy chain region.
KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KM humanised antibody; murine antigen binding region; inhibition;
KM leukocyte infiltration of tissue; treatment; inflammatory disease;
KM inflammatory bowel disease; ss.
OS Mus sp.
FH Key
FT Location/Qualifiers
FT CDS
FT 13..445
FT /tag- a
FT /note- "no stop codon given"
FT /transl_except- (pos: 16..18, aa: Xaa)
FT /transl_except- (pos: 19..21, aa: Xaa)
FT /transl_except- (pos: 22..24, aa: Xaa)
FT /transl_except- (pos: 25..27, aa: Xaa)
FT /transl_except- (pos: 28..30, aa: Xaa)
FT /transl_except- (pos: 31..33, aa: Ile)
FT /transl_except- (pos: 34..36, aa: Xaa)
FT /note- "Xaa- unknown"
FT 13..69
FT /tag- d
FT /tag- e
FT mat_peptide
FT 70..445
FT /tag- e
FT W09806248-A2.
FT 19-FEB-1998.
FT 06-AUG-1997; U13884.
FT 15-AUG-1996; US-700737.
FT (LEUK-) LEUKOSITE INC.
PI Bendig MW, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J,
PI WPI; 98-159172/14.
PI P-PSDB; W53816.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Example 1; Fig 1; 145pp; English.
CC The present sequence represents the consensus nucleotide sequence
CC comprising the variable region of murine Act-1 antibody determined from
CC several independent mouse heavy chain variable region clones. Act-1 is
CC active against human alpha4-beta7 integrin. Muscosal adressin cell
CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
CC MadCAM-1, which is present of high endothelial venules in muscosal
CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
CC produced several different sequences, of which the present sequence is a
CC consensus sequence. The present sequence was used to construct
CC chimeric, humanised Act-1 antibodies, which contain murine antigen
CC binding regions. The humanised immunoglobulin can be used to inhibit
CC the interaction of cells bearing alpha4-beta7 with cells bearing a
CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
CC infiltration of tissues, e.g. for treating inflammatory diseases such
CC as inflammatory bowel disease. The immunoglobulin can also be used for
CC detection, isolation and diagnosis.
SQ Sequence 494 BP; 113 A; 120 C; 118 G; 104 T;

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Query Match 99.1%; Score 416.4; DB 1; Length 494;
Best Local Similarity 97.9%; Pred. No. 5.2e-108;
Matches 411; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGATGGAGCTGTATATCTCTCTTGTGTATCAACAGCTCAAGTGTCCACTCCAG 60
|
|
|
Db 13 ATGRRATGSASCRKRRKATYYTCTTGTGTATCAACAGCTCAAGTGTCCACTCCAG 72
|
|
|
QY 61 GTCCAACTGCAAGCAGCTGGGGCTGAGCTTGTGAAGCTTGGAGTCAAGAGCTGCC 120
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|
|
Db 73 GTCCAACTGCAAGCAGCTGGGGCTGAGCTTGTGAAGCTTGGAGTCAAGAGCTGCC 132
|
|
|
QY 121 TGCAGAGGTTATGCTACCTTACACAGTACTGATGATGATGAGTGAAGAGAGGCT 180
|
|
|
Db 133 TGCAGAGGTTATGCTACCTTACACAGTACTGATGATGATGAGTGAAGAGAGGCT 192
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|
|
QY 181 GGACAGAGCCTTGTAGTGTGAGAGATTTGATCTTCTGAGAGTAACTAACTACAT 240
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|
|
Db 193 GGACAGAGCCTTGTAGTGTGAGAGATTTGATCTTCTGAGAGTAACTAACTACAT 252
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|
QY 241 CAAATTCAGAGGCAAGCCATTCAGTGTAGACATTTCTCAGACACCTACATG 300
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|
|
Db 253 CAAATTCAGAGGCAAGCCATTCAGTGTAGACATTTCTCAGACACCTACATG 312
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|
|
QY 301 CAGCTCAGACGCTGACATCTGAGAGACTCTGGGCTCTACTATTGTGCAAGGGGGTTAC 360
|
|
|
Db 313 CAGCTCAGACGCTGACATCTGAGAGACTCTGGGCTCTACTATTGTGCAAGGGGGTTAC 372
|
|
|
QY 361 GAGGATGGGACTATGCTATGACTAGTGGGCTCAAGGACCTCAGTCACCGTCTCCCA 420
|
|
|
Db 373 GAGGATGGGACTATGCTATGACTAGTGGGCTCAAGGACCTCAGTCACCGTCTCCCA 432
|
|
|
RESULT 3
V20089
ID V20089 standard; DNA; 428 BP.
AC V20089;
DT 14-JUL-1998 (first entry)
DE DNA sequence of murine variable heavy chain region of clone H2B#34.
KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KM humanised antibody; murine antigen binding region; inhibition;
KM leukocyte infiltration of tissue; treatment; inflammatory disease;
KM inflammatory bowel disease; ss.
OS Mus sp.
FH Key
FT Location/Qualifiers
FT CDS
FT 18..428
FT /tag- a
FT /note- "no stop codon given"
FT W09806248-A2.
FT 19-FEB-1998.
FT 06-AUG-1997; U13884.
FT 15-AUG-1996; US-700737.
FT (LEUK-) LEUKOSITE INC.
PI Bendig MW, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J,
PI WPI; 98-159172/14.
PI P-PSDB; W53816.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Example 1; Fig 2; 145pp; English.
CC The present sequence represents the nucleotide sequence comprising the
CC variable region of murine Act-1 antibody determined from clone H2B#34.
CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin
CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
CC to MadCAM-1, which is present of high endothelial venules in muscosal
CC lymph nodes. The present sequence was used to construct chimeric,
CC humanised Act-1 antibodies, which contain murine antigen binding regions.
CC The humanised immunoglobulin can be used to inhibit the interaction of

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CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
CC It can be used for inhibiting leukocyte infiltration of tissues, e.g., for
CC treating inflammatory diseases such as inflammatory bowel disease. The
CC immunoglobulin can also be used for detection, isolation and diagnosis.
SQ Sequence 428 BP; 108 A; 104 C; 115 G; 101 T;

Query Match 96.7%; Score 406.2; DB 1; Length 428;
Best Local Similarity 99.3%; Pred. No. 3.6e-105;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGATGAGCTGTATCATCTCTTCTTGTATCAACAGCTCAAGTGTCCCTCCAG 60
DB 18 ATGGATGAGCTGTATCATCTCTTCTTGTATCAACAGCTCAAGTGTCCCTCCAG 77
QY 61 GTCCAACTGACAGAGCTGGGCTGGAGCTGTAGAGCTGGAGCTCAAGTGTCTC 120
DB 78 GTCCAACTGACAGAGCTGGGCTGGAGCTGTAGAGCTGGAGCTCAAGTGTCTC 137
QY 121 TGCAGAGGTTATGGCTACACCTTACACAGCTAGTGCATGCTGGTGAAGAGAGGCTT 180
DB 138 TGCAGAGGTTATGGCTACACCTTACACAGCTAGTGCATGCTGGTGAAGAGAGGCTT 197
QY 181 GGCAGAGGCTTATGATGATCGAGAGATTTGATCTTGTAGAGTAACTAATCAAT 240
DB 198 GGCAGAGGCTTATGATGATCGAGAGATTTGATCTTGTAGAGTAACTAATCAAT 257
QY 241 CAAAAATTCAGAGGCAAGGCAATGACATGACATGACATGACATGACATGACATGAC 300
DB 258 CAAAAATTCAGAGGCAAGGCAATGACATGACATGACATGACATGACATGACATGAC 317
QY 301 CAGCTCAGAGCTGATCATCTGAGAGCTGCGGCTACTATTTGTGCAAGAGGCTTAC 360
DB 318 CAGCTCAGAGCTGATCATCTGAGAGCTGCGGCTACTATTTGTGCAAGAGGCTTAC 377
QY 361 GACGATGGAGTATCTTATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
DB 378 GACGATGGAGTATCTTATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428

RESULT 4

V20076 4
ID V20076 standard; DNA; 540 BP.
AC V20076;
DE 14-JUL-1998 (first entry)
KW DNA encoding the heavy chain of a humanised murine Act-1 antibody.
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MacdAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease; ss.
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
FH Homo sapiens.
FT Key
FT CDS
FT sig_peptide
FT mat_peptide
FT sig_peptide
FT mat_peptide
PD 19-FEB-1998.
PF 06-AUG-1997; 013884.
PR 15-AUG-1996; 05-700737.
PA (LEUK-) LEUKOSITE INC.
PI Bendish MM, Jones ST, Newman W, Ponath PD, Rungler DJ,
DR Saldaña J.
DR MPI: 98-159172/14.
DR P-PSDB; W53813.
PR Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -

PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Claim 22; Fig 11; 145pp; English.
CC The present sequence encodes the heavy chain of humanised murine
CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
CC Muscosal adressin cell adhesion molecule-1 (MacdAM-1) is a ligand of
CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
CC integrin binding to MacdAM-1, which is present of high endothelial
CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
CC used to inhibit the interaction of cells bearing alpha4-beta7 with
CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leukocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.

SQ Sequence 540 BP; 120 A; 150 C; 150 G; 120 T;

Query Match 85.5%; Score 359.2; DB 1; Length 540;
Best Local Similarity 91.0%; Pred. No. 5.7e-92;
Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGGATGAGCTGTATCATCTCTTCTTGTATCAACAGCTCAAGTGTCCCTCCAG 60
DB 1 ATGGATGAGCTGTATCATCTCTTCTTGTATCAACAGCTCAAGTGTCCCTCCAG 60
QY 61 GTCCAACTGACAGAGCTGGGCTGGAGCTGTAGAGCTGGAGCTCAAGTGTCTC 120
DB 61 GTCCAACTGACAGAGCTGGGCTGGAGCTGTAGAGCTGGAGCTCAAGTGTCTC 120
QY 121 TGCAGAGGTTATGGCTACACCTTACACAGCTAGTGCATGCTGGTGAAGAGAGGCTT 180
DB 121 TGCAGAGGTTATGGCTACACCTTACACAGCTAGTGCATGCTGGTGAAGAGAGGCTT 180
QY 181 GGCAGAGGCTTATGATGATCGAGAGATTTGATCTTGTAGAGTAACTAATCAAT 240
DB 181 GGCAGAGGCTTATGATGATCGAGAGATTTGATCTTGTAGAGTAACTAATCAAT 240
QY 241 CAAAAATTCAGAGGCAAGGCAATGACATGACATGACATGACATGACATGACATGAC 300
DB 241 CAAAAATTCAGAGGCAAGGCAATGACATGACATGACATGACATGACATGACATGAC 300
QY 301 CAGCTCAGAGCTGATCATCTGAGAGCTGCGGCTACTATTTGTGCAAGAGGCTTAC 360
DB 301 CAGCTCAGAGCTGATCATCTGAGAGCTGCGGCTACTATTTGTGCAAGAGGCTTAC 360
QY 361 GACGATGGAGTATCTTATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 GACGATGGAGTATCTTATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

RESULT 5

O94037 5
ID O94037 standard; CDNA; 1582 BP.
AC O94037;
DE 21-NOV-1995 (first entry)
KW MAb 55.1 heavy chain CDNA.
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin; ss.
OS Mus sp.
FH Homo sapiens.
FT Key
FT CDS
FT sig_peptide
FT mat_peptide
FT sig_peptide
FT mat_peptide
PD 08-JUN-1995.
PF 08-NOV-1994; G02610.
PR 03-DEC-1993; GB-024819.

PR 03-JUN-1994; GB-011089.
 PA (ZENE) ZENECA LTD.
 PI Blakey DC; Boot C; Copley CG, Hall SM, Paterson DS;
 PI Rose MS; Wright AF;
 DR WPI; 95-21562/28.
 P-PSDB: R76088.
 PT Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 PS disclosure: Fig.15; 13pp: English.
 CC Mab 55.1 (E6ACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. CDNA for the heavy (094037) and light (094036)
 CC chains of 55.1 were isolated, and F(ab)'₂, Fab, Fv, scFv or
 CC V-mun humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 SQ Sequence 1582 BP; 405 A; 466 C; 379 G; 332 T;

Query Match 80.0%; Score 335.8; DB 1; Length 1582;
 Best Local Similarity 87.6%; Pred. No. 2,8e-85;
 Matches 367; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 ATGGAGTGGAGCTGTATCATCTCTTCTTGTGTATCAACAGCTAAATGTCCACTCCAG 60
 DB 54 ATGGAGTGGAGCTGTATCATCTCTTCTTGTGTATCAACAGCTAAATGTCCACTCCAG 113
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTGTGAAGCTGTCC 120
 DB 114 GTCCAACTGCAGCAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTGTGAAGCTGTCC 173
 QY 121 TGCAGAGGTTATGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 180
 DB 174 TGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 233
 QY 181 GGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 240
 DB 234 GGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 293
 QY 241 CAAATATTCAGAGGCAAGGCACTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 300
 DB 294 GAGAGGTTCAAGAGCAAGGCACTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 353
 QY 301 CAGCTCAGCAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 360
 DB 354 CAGCTCAGCAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 413
 QY 361 GAGGAGTGGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 419
 DB 414 TATGTTACGACGATGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 472

RESULT 6
 Q15164
 ID Q15164 standard; DNA; 458 BP.
 AC Q15164;
 DT 16-MAR-1992 (first entry)
 DE VHL86 region of anti-nitrophenylacetyl heavy chain Ab gene.
 KM mouse; murine; antibody; heavy chain; variable region;
 KM polymerase chain reaction; ss.
 OS Mus musculus.
 PN J03247283-A.
 PD 05-NOV-1991.
 PF 29-DEC-1989; 340628.
 PR 29-DEC-1989; JP-340628.
 PA (MAYO) MATSUSHITA ELEC IND KK.
 DR WPI; 91-366330/50.
 PT DNA binding to terminal of anti-nitrophenylacetyl antibody gene
 PT - allows specific amplification of variable region in gene by PCR
 PS disclosure: Page 2; 3pp: Japanese.
 CC This sequence corresponds to the region of the heavy chain variable
 CC region of the murine anti-nitrophenylacetyl IgG antibody which is
 CC amplified by PCR primers HA and HS.
 CC See Q15159-Q15163.

SQ Sequence 458 BP; 112 A; 124 C; 120 G; 102 T;

Query Match 78.7%; Score 330.4; DB 1; Length 458;
 Best Local Similarity 88.3%; Pred. No. 6.4e-84;
 Matches 371; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 ATGGAGTGGAGCTGTATCATCTCTTCTTGTGTATCAACAGCTAAATGTCCACTCCAG 60
 DB 1 ATGGAGTGGAGCTGTATCATCTCTTCTTGTGTATCAACAGCTAAATGTCCACTCCAG 60
 QY 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTGTGAAGCTGTCC 120
 DB 61 GTCCAACTGCAGCAGCTGGGGCTGAGCTTGTGAAGCTGGAGCTTGTGAAGCTGTCC 120
 QY 121 TGCAGAGGTTATGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 180
 DB 121 TGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 180
 QY 181 GGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 240
 DB 181 GGCAGAGGCTTGTGCTTACCTTACCTTACAGCTTGTGATGAGCTGGTGAAGAGGCT 240
 QY 241 CAAATATTCAGAGGCAAGGCACTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 300
 DB 241 GAGAGGTTCAAGAGCAAGGCACTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 300
 QY 301 CAGCTCAGCAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 360
 DB 301 CAGCTCAGCAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 360
 QY 361 GAGGAGTGGAGCTTGTGATGAGCTTGTGATGAGCTTGTGATGAGCTGGTGAAGAGGCT 420
 DB 361 TACGTTAGTACGTA---CTTGTACTGTGGGCAAGGCAAGCAGCTTGTGATGAGCTGGTGAAGAGGCT 417

RESULT 7
 T05312
 ID T05312 standard; DNA; 429 BP.
 AC T05312;
 DT 02-FEB-1996 (first entry)
 DE Mab SCH94.03 heavy chain DNA.
 KM Monoclonal antibody; Mab; SCH94.03; hybridoma; central nervous system;
 KM CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
 KM ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT cds 1..429
 FT signal_peptide 1..57
 FT mat_peptide 58..429
 FT /tag= a
 FT /tag= b
 FT /tag= c
 PN W09530004-A1.
 PD 09-NOV-1995.
 PF 27-APR-1995; U05262.
 PR 29-APR-1994; US-236520.
 PA (MAYO-) MAYO FOUNDATION.
 PI Miller DJ, Rodriguez M;
 DR WPI; 95-393077/50.
 P-PSDB: R84554.
 PT Monoclonal antibodies which stimulate central nervous system
 PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
 PT treating multiple sclerosis, and viral or post-neural diseases of
 PT the CNS.
 PS disclosure: Page 38; 63pp: English.
 CC Hybridoma ATCC CRL 11627 was obtained from a SJL/J mouse injected with
 CC spinal cord homogenate from a mammal uninfected with any
 CC demyelinating disease. The hybridoma produced a monoclonal antibody
 CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
 CC heavy chain germline sequence is given in T05312.
 SQ Sequence 429 BP; 109 A; 111 C; 113 G; 96 T;

Db 386 GACTGCT-----TTGCTTACTGGGCGCAAGGACTCTGTGTCACCGTCTCTCA 433

RESULT 11

AC T36304 standard; cDNA; 420 BP.

AC T36304;

DT 21-OCT-1997 (first entry)

DE Anti-hepatitis B heavy chain variable region cDNA in pING2012E.

KW Immunoglobulin G; IgG; heavy chain; recombinant production;

KW antibody; passive immunisation; serum sickness; anaphylactic shock;

KW immunoassay; imaging; reagent; complement mediated lysis;

KW therapy; hepatitis B virus; variable region; HBV; ss.

OS Mus spp.

FT Key

FT mat_peptide 13.420

FT /*tag- a

PN US595898-A.

PD 21-JAN-1997.

PF 01-NOV-1985; 793980.

PR 29-MAR-1990; US-501092.

PR 01-NOV-1985; US-793980.

PR 27-OCT-1986; WO-002269.

PR 24-JUL-1987; US-077528.

PR 11-JAN-1988; US-142039.

PR 08-DEC-1992; US-987555.

PR 18-AUG-1994; US-299085.

PA (XOMA) XOMA CORP.

PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR;

PI Wall R, Wilcox GL;

DR WPI: 97-107579/10.

DR P-SDB: W10584.

PT Nucleic acid encoding immunoglobulin fragment - comprising

PS dielctronic transcription unit with pectate lyase signal sequences

PS Example; Fig 12B; 98pp; English.

CC The present sequence is the anti-hepatitis B heavy chain variable

CC region cDNA in pING2012E, which was used in the preparation of a

CC novel polynucleotide molecule encoding an Ig fragment. The DNA

CC molecule comprises 2 DNA sequences encoding 2 pectate lyase

CC secretion signal sequences respectively linked to a DNA sequence

CC encoding an Ig Fd molecule or Ig light chain, operably linked to a

CC single prokaryotic promoter so as to form a dielctronic

CC transcription unit, provided that the Ig fragment can bind an

CC antigen and is produced and secreted by an E. coli host cell when

CC the nucleic acid molecule is expressed in the host cell.

CC The polynucleotide molecule is used for the production of

CC recombinant antibodies, which can be used for passive immunisation

CC without negative immune reactions (e.g. serum sickness and

CC anaphylactic shock). In labelled forms as immunoassay or imaging

CC reagents, in complement mediated lysis and for therapeutic

CC purposes when coupled to a toxin or other therapeutic agent.

SQ Sequence 420 BP; 102 A; 109 C; 110 G; 99 T;

Query Match 71.0%; Score 298; DB 1; Length 420;

Best Local Similarity 84.0%; Pred. No. 7.4e-75;

Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGATATATCTCTCTTGTGATACAGCTACAGTGCATCCAG 60

DB 13 ATGGATGAGCTATATATCTCTCTTGTGATACAGCTACAGTGCATCCAG 72

QY 61 GTCCAACTGACAGAGCTGGGGCTGAGCTTGGAAGCTGGGACTTCAGTGAAGTGC 120

DB 73 GTCCAACTGACAGAGCTGGGGCTGAGCTTGGAAGCTGGGACTTCAGTGAAGTGC 132

QY 121 TCGAAGGTTATGGCTACACCTTCACAGCTACTGATGACATGGGTGAAGAGAGGCT 180

DB 133 TCGAAGGCTCTGGCTACACCTTCACAGCTACTGATGACATGGGTGAAGAGAGGCT 192

QY 181 GGACAGGCTTGAAGTGAAGAGATGATCTCTTGTGAGAGTAATACACTACAT 240

DB 193 GGACAGGCTTGAAGTGAAGAGATGATCTCTTGTGAGAGTAATACACTACAT 252

QY 241 CAAAATTCAGAGGCGCAGCCATTTGATGACATTTCTCCAGCAGACCTACATG 300

DB 253 GAGAAGTTCAGAGGCGCAGCCATTTGATGACATTTCTCCAGCAGACCTACATG 312

QY 301 CAGCTCAGCAGCCTGACATCTGAGACTCTCGGCTCTACTATTTGTCAGAGGGGTTAC 360

DB 313 CAGCTCAGCAGCCTGACATCTGAGACTCTCGGCTCTACTATTTGTCAGAGGGGTTAC 372

QY 361 GAGGATGGAGCTATGATGACACTGGGGTCAAGGCACTGATGACCTGCTCCCA 420

DB 373 GACTGCT-----TTGCTTACTGGGCGCAAGGACTCTGTGTCACCGTCTCTCA 420

RESULT 12

AC V18553 standard; DNA; 420 BP.

AC V18553;

DT 05-JUN-1998 (first entry)

DE Human anti-hepatitis antibody heavy chain gene in pING2012E.

KW Mouse; murine; human anti-hepatitis antibody; heavy chain;

KW Immunoglobulin fragment production; Ig fragment production;

KW monoclonal antibody L6; human lung carcinoma cell;

OS Homo sapiens.

OS Synthetic.

FT Key

FT mat_peptide 13.433

FT /*tag- a

PN US5698435-A.

PD 16-DEC-1997.

PF 06-JUN-1995; 467140.

PR 29-MAR-1990; US-501092.

PR 01-NOV-1985; US-793980.

PR 27-OCT-1986; WO-002269.

PR 24-JUL-1987; US-077528.

PR 11-JAN-1988; US-142039.

PR 08-DEC-1992; US-987555.

PR 18-AUG-1994; US-299085.

PR 06-JUN-1995; US-467140.

PA (XOMA) XOMA CORP.

PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,

PI Wall R, Wilcox GL;

DR WPI: 98-051492/05.

DR P-SDB: W47510.

PT DNA encoding secretable immunoglobulin fragments - comprising at

PS least the variable regions of light or heavy chains

PS Example II; Fig 12B; 98pp; English.

CC The present sequence was used in the development of a novel method

CC for the production of an immunoglobulin (Ig) fragment capable of

CC binding an antigen. The method comprises culturing an E. coli host

CC that has been transformed with a nucleic acid molecule encoding the

CC Ig fragment, under conditions so that the Ig fragment is produced

CC and secreted. The nucleic acid molecule comprises DNA sequences

CC encoding: (a) pectate lyase secretion signal sequence operably

CC linked to a DNA sequence encoding at least the variable region of

CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence

CC operably linked to a DNA sequence encoding at least the variable

CC region of an Ig light chain, where (a) and (b) are operably linked

CC to a single prokaryotic promoter to form a dielctronic

CC transcription unit. The method is used to produce chimeric Fab

CC molecules, e.g. derived from murine monoclonal antibody L6 raised

CC against human lung carcinoma cells. The invention provides a novel

CC approach for producing genetically engineered antibodies of

CC desired variable region specificity and constant region

CC properties. The cloned Ig gene products can be produced by

CC expression in genetically engineered organisms. The application of

CC chemical gene synthesis, recombinant DNA cloning and production of

CC specific Ig chains in various organisms provides an effective

CC solution for the efficient large scale production of human

CC monoclonal antibodies. The invention also provides a solution to

CC the problem of class switching antibody molecules.

SQ Sequence 420 BP; 102 A; 109 C; 110 G; 99 T;

Query Match 71.0%; Score 298; DB 1; Length 420;
 Best Local Similarity 84.0%; Pred. No. 7.4e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGATCATCTCTCTTGGTATCAACAGCTACAGTGTCCATCCAG 60
 DB 13 ATGGATGAGCTGATCATCTCTCTTGGTATCAACAGCTACAGTGTCCATCCAG 72
 QY 61 GTCCACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120
 DB 73 GTCCACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 132
 QY 121 TGCAGAGGTTATGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 180
 DB 133 TGCAGAGGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 192
 QY 161 GGACAGAGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 240
 DB 193 GGACAGAGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 252
 QY 241 CAAATATTCAGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 300
 DB 253 GGAAGCTTCAGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 312
 QY 301 CAGCTCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 360
 DB 313 CAGCTCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 372
 QY 361 GACGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 420
 DB 373 GACTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 420

RESULT 13:
 V18554 standard; DNA: 433 BP.
 AC V18554:
 DT 05-JUN-1998 (first entry)
 DE Human anti-hepatitis antibody heavy chain gene in PING2006E.
 KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
 KW Immunoglobulin fragment production; Ig fragment production;
 KW Monoclonal antibody L6; human lung carcinoma cell;
 KW PING2006E; ss.
 OS Homo sapiens.
 OS Synthetic.
 FT Key location/Qualifiers
 FT mat_peptide 26..433
 FT /*tag= a

US5698435-A.
 PD 16-DEC-1997.
 PF 06-JUN-1995; US-501092.
 PR 29-MAR-1980; US-501092.
 PR 01-NOV-1985; US-793980.
 PR 27-OCT-1986; WO-002269.
 PR 24-JUL-1987; US-077528.
 PR 11-JAN-1988; US-142039.
 PR 08-DEC-1992; US-987555.
 PR 18-AUG-1994; US-299085.
 PR 06-JUN-1995; US-467140.
 PA (XOMA) XOMA CORP.
 PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
 PI Wall R, Wilcox GL,
 DR WPI: 98-051492/05.
 DR P-PSDB: W47510.
 PT DNA encoding secretable immunoglobulin fragments - comprising at
 PT least the variable regions of light or heavy chains
 PS Example II; Fig 12B; 98pp; English.
 CC The present sequence was used in the development of a novel method
 CC for the production of an immunoglobulin (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing an E. coli host
 CC that has been transformed with a nucleic acid molecule encoding the

CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. The nucleic acid molecule comprises DNA sequences
 CC encoding: (a) pectate lyase secretion signal sequence operably
 CC linked to a DNA sequence encoding at least the variable region of
 CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
 CC operably linked to a DNA sequence encoding at least the variable
 CC region of an Ig light chain, where (a) and (b) are operably linked
 CC to a single prokaryotic promoter to form a dicistronic
 CC transcription unit. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody L6 raised
 CC against human lung carcinoma cells. The invention provides a novel
 CC approach for producing genetically engineered antibodies of
 CC desired variable region specificity and constant region
 CC properties. The cloned Ig gene products can be produced by
 CC expression in genetically engineered organisms. The application of
 CC chemical gene synthesis, recombinant DNA cloning and production of
 CC specific Ig chains in various organisms provides an effective
 CC solution for the efficient large scale production of human
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 CC Sequence 433 BP; 102 A; 126 C; 108 G; 97 T;

Query Match 71.0%; Score 298; DB 1; Length 433;
 Best Local Similarity 84.0%; Pred. No. 7.5e-75;
 Matches 353; Conservative 0; Mismatches 55; Indels 12; Gaps 1;

QY 1 ATGGATGAGCTGATCATCTCTCTTGGTATCAACAGCTACAGTGTCCATCCAG 60
 DB 26 ATGGATGAGCTGATCATCTCTCTTGGTATCAACAGCTACAGTGTCCATCCAG 85
 QY 61 GTCCACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 120
 DB 86 GTCCACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 145
 QY 121 TGCAGAGGTTATGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 180
 DB 146 TGCAGAGGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 205
 QY 181 GGACAGAGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 240
 DB 206 GGACAGAGCTTGTGCTTACACCTTTCACAGCTGAGCTGAGCTGAGCTGAGCTGAG 265
 QY 241 CAAATATTCAGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 300
 DB 266 GGAAGCTTCAGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 325
 QY 301 CAGCTCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 360
 DB 326 CAGCTCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 385
 QY 361 GACGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 420
 DB 386 GACTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 433

RESULT 14:
 V03866 standard; DNA: 433 BP.
 AC V03866:
 DT 01-JUN-1998 (first entry)
 DE Human anti-hepatitis antibody heavy chain gene in PING2006E.
 KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
 KW Immunoglobulin fragment production; Ig fragment production;
 KW Monoclonal antibody L6; human lung carcinoma cell;
 KW PING2006E; ss.
 OS Homo sapiens.
 OS Synthetic.
 FT Key location/Qualifiers
 FT mat_peptide 26..433
 FT /*tag= a

US5693493-A.
 PD 02-DEC-1997.

PE 25-MAY-1995; 4450731.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980
PR 27-OCT-1986; WO-002269
PR 24-OUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PA (XOMA) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
PI WPI: 98-031749/03.
DR P-PSDB; W41054.
PR production of chimeric antibody fragments - by culturing E. coli
PI transformed with chimeric expression cassette
PS Example II: Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule, and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 16 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 433 BP; 102 A; 126 C; 108 G; 97 T;

Query Match	71.0%	Score 298	DB 1	Length 433
Best Local Similarity	84.0%	Pred. No. 7.5e-75		
Matches 353	Conservative 0	Mismatches 55	Indels 12	Gaps 1
Qy	1	ATGGATGAGCTGATTCATCTCTCTCTGGTTCACAGCTTCAGATGTCACCTCCAG	60	
Db	26	ATGGATGAGCTATATCATCTCTCTTTGGTAGCAGACGCTTGAATGTCACCTCCAG	85	
Qy	61	GTCCAACTCAGACAGCCTGGGCGTAGCTTGTAAGCCTGGGACTCAGTGAAGCTGAC	120	
Db	86	GTCCAATTCCAGCAGCCTGGGCGTAGCTTGTAAGCCTGGGCTTCAGTGAAGCTGAC	145	
Qy	121	TGCAGGGTTATGGCTACACCTTCACACGCTACTGGATGCATCGGGGTGAAGCAGGCT	180	
Db	146	TGCAGGCTCTGGCTACACCTTCACACGCTACTGGATGCATCGGGGTGAAGCAGGCT	205	
Qy	181	GGACAAGCCTTGAGTGCATCGAGAGATTGATCTTGTAGAGTAACTACTACTCAAT	240	
Db	206	GGACAAGCCTTGAGTGCATCGAGAGATTGATCTTGTAGAGTAACTACTACTCAAT	265	
Qy	241	CAAAAATTCAAGGGCAGAGCCACATTGACTGTAGACATTTCTCCAGCAGAGCCTACATG	300	
Db	266	GAGAACTCAAGAGCAGAGCCACACTGACTGTAGACAAATCTCCAGCAGAGCCTACATG	325	
Qy	301	CAGCTCAGACGCTGCATCTGAGAGACTCTGGGTCTACTATTGTGCAGAAGGGGGTTAC	360	
Db	326	CAGCTCAGACGCTGCATCTGAGAGACTCTGGGTCTACTATTGTGTGCTCTCTATGATAC	385	
Qy	361	GACGATGGGACATCTCTATGACTACTGGGGTCAAGGACCTCAATCACTCTCTCTTA	420	

Db	386	GACGCGT-----TTGCTACTAGGGGCCAAGACACTCTGCGACCGTCTCTCA	433
RESULT	15		
ID	V03836		
AC	V03836 standard; DNA; 420 BP.		
DC	01-JUN-1998 (first entry)		
DE	Human anti-hepatitis antibody heavy chain gene in pING2012E.		
KW	Mouse; murine; human anti-hepatitis antibody; heavy chain; immunoglobulin fragment production; Ig fragment production; monoclonal antibody L6; human lung carcinoma cell; pING2012E; ss.		
OS	Homo sapiens.		
FT	Synthetic.		
FT	Key	Location/Qualifiers	
FT	mat_peptide	13..433	
FT		/*tag= a	
PN	US5693493-A.		
PD	02-DEC-1997.		
PF	23-MAY-1995; 450731.		
PR	29-MAR-1990; US-501092.		
PR	01-NOV-1985; US-793980.		
PR	27-OCT-1986; WO-003269.		
PR	24-JUL-1987; US-077528.		
PR	11-JAN-1988; US-142039.		
PR	08-DEC-1992; US-987555.		
PR	18-AUG-1994; US-299085.		
PR	23-MAY-1995; US-450731.		
PA	(XOMA) XOMA CORP.		
PI	Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,		
PI	Wall R, Wilcox GL,		
PI	WPI: 98-031749/03.		
PR	P-PSDB: W41054.		
PT	Production of chimeric antibody fragments - by culturing E. coli		
PS	transformed with dicistronic expression cassette		
PT	Example II: Fig 12b: 98pp: English.		
CC	The present sequence was used in the development of a novel method		
CC	for the production of an immunoglobulin (Ig) fragment capable of		
CC	binding an antigen. The method comprises culturing an E. coli host		
CC	cell that has been transformed with a nucleic acid molecule encoding the		
CC	Ig fragment, under conditions so that the Ig fragment is produced		
CC	and secreted. The nucleic acid molecule comprises DNA sequences		
CC	encoding: (a) pectate lyase secretion signal sequence operably		
CC	linked to a DNA sequence encoding at least the variable region of		
CC	an Ig Fd molecule; and (b) pectate lyase secretion signal sequence		
CC	operably linked to a DNA sequence encoding at least the variable		
CC	region of an Ig light chain, where (a) and (b) are operably linked		
CC	to a single prokaryotic promoter to form a dicistronic		
CC	transcription unit. The method is used to produce chimeric Fab		
CC	molecules, e.g. derived from murine monoclonal antibody L6 raised		
CC	against human lung carcinoma cells. The invention provides a novel		
CC	approach for producing genetically engineered antibodies of		
CC	desired variable region specificity and constant region		
CC	properties. The cloned Ig gene products can be produced by		
CC	expression in genetically engineered organisms. The application of		
CC	chemical gene synthesis, recombinant DNA cloning and production of		
CC	specific Ig chains in various organisms provides an effective		
CC	solution for the efficient large scale production of human		
CC	monoclonal antibodies. The invention also provides a solution to		
CC	the problem of class switching antibody molecules.		
Sequence	420 BP; 102 A; 109 C; 110 G; 99 T;		

Query Match	71.0%	Score 298	DB 1	Length 420
Best Local Similarity	84.0%	Pred. No. 7	4e-75	
Matches 353	Conservative 0	Mismatches 55	Indels 12	Gaps 1
QY	1	ATGGATGAGCTGTATCATCTCTCTTTTGGTATCAACAGCTTACAGTGTCCACTCCAG	60	
DB	13	ATGGATGAGCTATATCATCTCTTTTGGTATCAACAGCTTACAGTGTCCACTCCAG	72	

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OY 61 GTCCAACTGCAGACGCTGGGGCTGAGCTTGTAAGCCTGGGACTTCAGTGAAGCTGTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 GTCCAAATTGCAGACGCTGGGGCTGAACTGGTAACCTGGGCTTCAGTGAAGTGTCC 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 TGCAGGGTTATGGCTACACCTTCACCAAGCTACTGATGCACCTGGGTGAAGCAGAGGCT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133 TGCAGGGCTCTGTGCTACACCTTCACCAAGCTACTGATGCACCTGGGTGAAGCAGAGGCT 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 GGACAAGGCTTGTAGTGGATCGAGAGATGATTCCTTGTAGAGTAATTAATACTACAAAT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 GGACAAGGCTTGTAGTGGATCGAGAGATGATTCCTTGTAGAGTAATTAATACTACAAAT 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 CAAAATTCAAGGGCAAGGCCACATTTGACTGTAGACATTTCTCCAGCAGACCTACATG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 GAGAAGTTCAAGAGCAAGGCCACACTGACTAGACAAATCCTCCAGCAGACCTACATG 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 CAGCTCAGACGCTGACATCTGAGGACTCTGGCTCTACTATTTGCAAGAGGGGTTAC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 313 CAACCTCAGACGCTGACATCTGAGGACTCTGGCTCTACTATTTGCAAGAGGGGTTAC 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 361 GACGGATGGGACTATGCTATTTGACTACTGGGGTCAAGGCACTCAGTCACCGTCTCTCA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 GACTGGT-----TTGCTTACTGGGGCCAAGGACTCTGTGTCACCGTCTCTCA 420
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Job time: 1536 sec

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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:23:24 ; Search time 30.48 Seconds
(without alignments)
172.062 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGMWDYIDYWGQSTSVTVSS 140

Scoring table: BLOSUM62

Searched: 116738 seqs, 37460341 residues

Database : PIR_58:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	603	79.7	138	2	E32513	Ig heavy chain pre
2	599.5	79.2	139	1	MHMS18	Ig heavy chain pre
3	592.5	78.3	141	2	JL0076	Ig heavy chain pre
4	579.5	76.6	135	2	A30577	Ig heavy chain pre
5	576	76.1	131	2	A27472	Ig heavy chain pre
6	559	73.8	138	1	HVMS17	Ig heavy chain pre
7	556	73.4	117	1	HVMS02	Ig heavy chain pre
8	555	73.3	136	2	B47155	Ig heavy chain pre
9	554.5	73.2	137	1	GZMS43	Ig heavy chain pre
10	552	72.9	136	2	PL0208	Ig heavy chain pre
11	551.5	72.9	137	2	E29380	Ig heavy chain pre
12	551.5	72.9	137	2	E29380	Ig heavy chain pre
13	546.5	72.2	136	2	JL0077	Ig heavy chain pre
14	543	71.7	117	1	HVMS3	Ig heavy chain pre
15	537	70.9	117	1	HVMS61	Ig heavy chain pre
16	533.5	70.5	120	2	B22769	Ig heavy chain pre
17	533	70.4	140	2	PH1482	Ig heavy chain pre
18	532	70.3	140	1	HVMS07	Ig heavy chain pre
19	529.5	69.9	139	2	PS0024	Ig heavy chain pre
20	527.5	69.7	120	2	S41394	Ig heavy chain pre
21	527	69.6	117	1	HVMS24	Ig heavy chain pre
22	525	69.4	117	1	MHMSB4	Ig heavy chain pre
23	524	69.2	138	2	S21810	Ig heavy chain pre
24	523	69.1	116	2	184704	Ig heavy chain pre
25	520	68.7	140	2	PH1489	Ig heavy chain pre
26	519.5	68.6	116	2	S33751	Ig heavy chain pre
27	519	68.6	117	1	HVMS45	Ig heavy chain pre
28	518.5	68.4	139	2	A27609	Ig heavy chain pre
29	517.5	68.4	141	2	A39276	Ig heavy chain pre
30	517	68.3	140	2	PH1484	Ig heavy chain pre
31	515	68.0	123	2	S20646	Ig heavy chain pre
32	514.5	68.0	287	3	PC4402	Ig heavy chain pre
33	514	67.9	120	2	S25175	Ig heavy chain pre
34	511	67.5	140	2	PH1488	Ig heavy chain pre
35	509.5	67.3	137	2	H32513	Ig heavy chain pre
36	507	67.0	135	2	PH1493	Ig heavy chain pre
37	507	67.0	122	2	S20643	Ig heavy chain pre
38	506	66.8	140	2	PH1486	Ig heavy chain pre
39	506	66.8	140	2	PH1498	Ig heavy chain pre

40 505.5 66.8 469 2 S37483 Ig gamma-2a chain
41 504.5 66.6 150 2 PN0444 Ig heavy chain v r
42 503 66.4 140 2 A36194 Ig heavy chain v r
43 503 66.4 135 2 PH1492 Ig heavy chain v r
44 502.5 66.4 126 2 S31930 Ig gamma chain pre
45 500 66.1 140 2 S04575 Ig heavy chain pre

ALIGNMENTS

RESULT 1

E32513
Ig heavy chain precursor V region (MRL22) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998

C:Accession: E32513

R:Koller, R.; Ströhal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization a

A:Reference number: A94689; MUID:88331394

A:Accession: E32513

A:Molecule type: DNA

A:Residues: 1-138 <KOR>

A:Cross-References: GB:M20835; NID:G196945; PID:G196946

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 79.7%; Score 603; DB 2; Length 138;

Best Local Similarity 82.9%; Pred. No. 2.7e-45;

Matches 116; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVQLQPGALYKRGTSVKLSCKGYCTFTSYMMHWKORP 60

Db 1 MGWSCIILFLVAAATGVHSQVQLQPGALYKRGASVSKLSCKASGYCTFTSYMMHWKORP 60

QY 61 GQGLEWIGELDPESNTNOKFKRATLVDPISSTAYMQLSTSEDSAVYCARGY 120

Db 61 GQGLEWIGNITVPSSSTNNNEKRSKATLVDPISSTAYMQLSTSDSAVYTCARRL 120

QY 121 DGMWDYIDYWGQSTSVTVSS 140

Db 121 R-YAMDYWGQSTSVTVSS 138

RESULT 2

MHMS18
Ig heavy chain precursor V region (B1-8) - mouse

N:Contains: Ig heavy chain precursor V region 186-2

C:Species: Mus musculus (house mouse)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1992 #text_change 20-Mar-1998

C:Accession: A90809; B90809; A22769; A02034; A02036

R:Bothwell, A.L.M.; Paskind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore

Cell 24, 625-637, 1981

A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:

A:Reference number: A90809; MUID:81234548

A:Accession: A90809

A:Molecule type: DNA

A:Residues: 1-139 <B18>

A:Cross-References: GB:J00529; NID:G195114; PID:G195115

A:Accession: B90809

A:Molecule type: DNA

A:Residues: 1-117 <1862>

A>Note: The B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the h

A>Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA

A:Diridrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.

EMBO J. 1, 635-640, 1982

A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination betwe

A:Reference number: A90971; MUID:84236026

A:Accession: A22769

A:Molecule type: protein

A:Residues: 20-139 <DII>
 A:Note: the V region of the BI-8 delta chain, derived as a spontaneous class switch variant of the mu chain
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-139/Product: Ig kappa chain V region (BI-8) #status experimental <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:118-124/Region: D segment
 F:125-139/Region: J segment (JH2)

Query Match 79.2%; Score 599.5; DB 1; Length 139;
 Best Local Similarity 80.7%; Pred. No. 5.4e-45;
 Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGLLEWIGELIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDAVYYCARGGY 120
 DB 61 GGLLEWIGRIDPNSGGTCKNEKSKATLTVDKPSSTAYMQLSLTSEDAVYYCARXYD 120
 QY 121 DGMVDAIDYWGQGTSTVSS 140
 DB 121 YGSSY-FDYWGQGTTLTVSS 139

RESULT 3

Ig heavy chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
 C:Accession: J10076
 R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
 MOL. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive reference number: J10076; MUID:89096973
 A:Accession: J10076
 A:Molecule type: mRNA
 A:Residues: 1-141 <KAA>
 A:Cross-references: GB:M27788; NID:9195851; PID:9195852
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-141/Product: Ig heavy chain #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:50-54/Region: complementarity-determining 1
 F:69-85/Region: complementarity-determining 2
 F:123-135/Region: J2 segment
 F:136-141/Region: C

Query Match 78.3%; Score 592.5; DB 2; Length 141;
 Best Local Similarity 80.0%; Pred. No. 2.2e-44;
 Matches 112; Conservative 7; Mismatches 16; Indels 5; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGLLEWIGELIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDAVYYCARGGY 120
 DB 61 GGLLEWIGRIDPNSGGTCKNEKSKATLTVDKPSSTAYMQLSLTSEDAVYYCARREG 120
 QY 121 DGMVDAIDYWGQGTSTVSS 140
 DB 121 AG-----DYWGQGTTLTVSS 135

RESULT 4
 Ig heavy chain precursor V region (MRL10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
 C:Accession: A30577
 R:Koller, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
 J. Exp. Med. 161, 805-815, 1985
 A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
 A:Reference number: A30577; MUID:85159423
 A:Accession: A30577
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <KOP>
 A:Cross-references: GB:M37621
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 579.5; DB 2; Length 135;
 Best Local Similarity 78.9%; Pred. No. 2.7e-43;
 Matches 112; Conservative 8; Mismatches 13; Indels 9; Gaps 2;

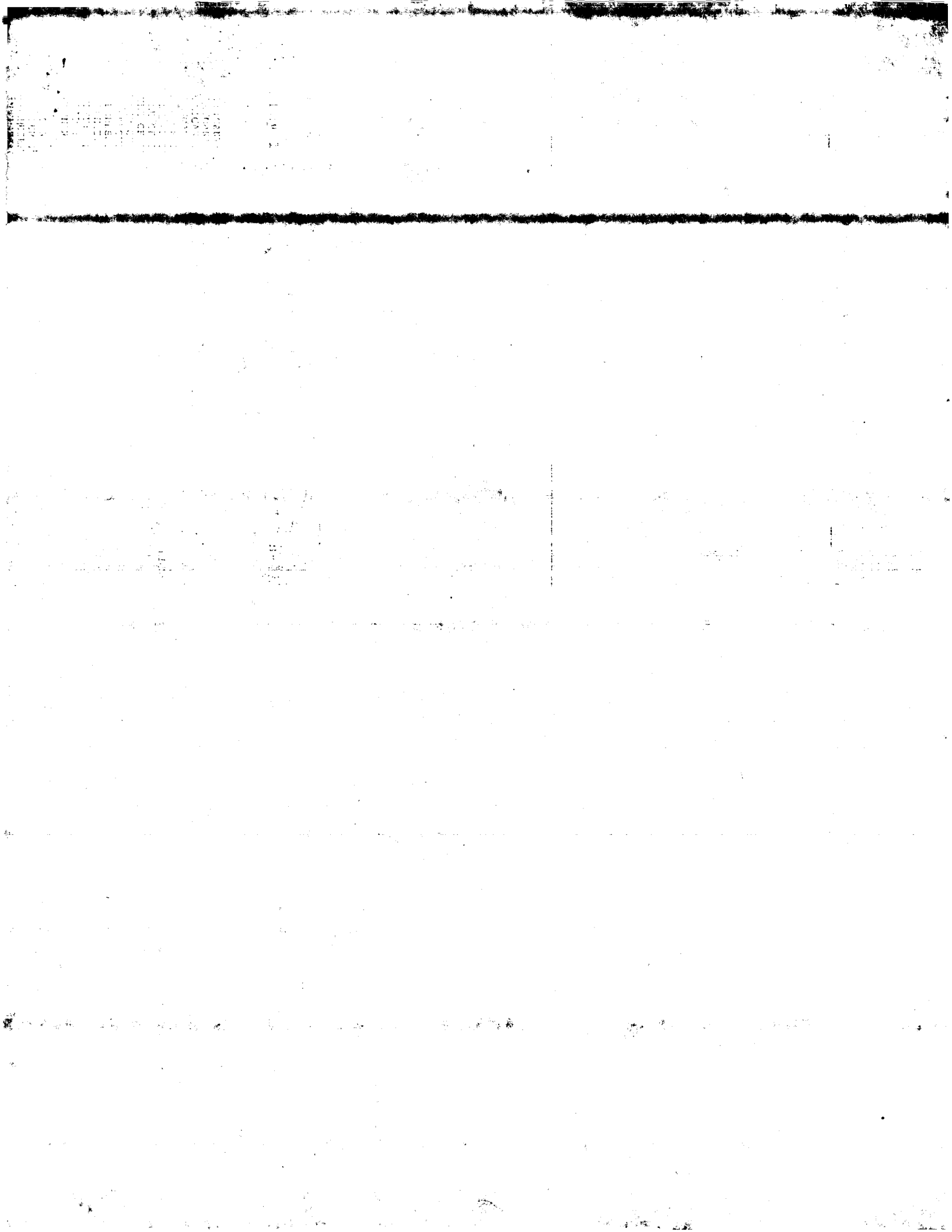
QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGLLEWIGELIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDAVYYCAR--G 118
 DB 61 GGLLEWIGRIDPNSGGTCKNEKSKATLTVDKPSSTAYMQLSLTSEDAVYYCARLWG 120
 QY 119 GYDGMVDAIDYWGQGTSTVSS 140
 DB 121 GF-----AYWGQGTTLTVSSA 135

RESULT 5

Ig heavy chain precursor V region (1E9) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996
 C:Accession: A27472
 R:Lin, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
 Gene 54, 33-40, 1987
 A:Title: Expression of mouse::human immunoglobulin heavy-chain cDNA in lymphoid cells
 A:Reference number: A27472; MUID:87277430
 A:Accession: A27472
 A:Molecule type: mRNA
 A:Residues: 1-131 <LID>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:5-54/Region: complementarity-determining 1
 F:20-131/Product: Ig heavy chain V region 1E9 #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:69-85/Region: complementarity-determining 2
 F:118-125/Region: complementarity-determining 3

Query Match 76.1%; Score 576; DB 2; Length 131;
 Best Local Similarity 82.8%; Pred. No. 5.3e-43;
 Matches 111; Conservative 4; Mismatches 15; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGWSCIILFLVSTATSVHSQVLOQPGAEIVKPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GGLLEWIGELIDPESNTNOKFKKATLTVDISSSTAYMQLSLTSEDAVYYCARGGY 120
 DB 61 GGLLEWIGELIDPESNTNOKFKKATLTVDKPSSTAYMQLSLTSEDAVYYCARSTYD 120
 QY 121 DGMVDAIDYWGQGT 134



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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:20:08 ; Search time 22.45 Seconds

(without alignments)
167,378 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MWMSCITFLVSTFATSVHSQ.....DGMVDAIDYWGQGTSTVYSS 140

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database: SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	599.5	79.2	139	1	HV07_MOUSE
2	559	73.8	138	1	HV08_MOUSE
3	556	73.4	117	1	HV06_MOUSE
4	554.5	73.2	137	1	HV11_MOUSE
5	543	71.7	117	1	HV05_MOUSE
6	537	70.9	117	1	HV09_MOUSE
7	532	70.3	140	1	HV02_MOUSE
8	527	69.6	117	1	HV04_MOUSE
9	525	69.4	117	1	HV09_MOUSE
10	519	68.6	117	1	HV10_MOUSE
11	497	65.7	136	1	HV15_MOUSE
12	479.5	63.3	120	1	HV50_MOUSE
13	468	61.8	120	1	HV03_MOUSE
14	447	59.0	121	1	HV01_MOUSE
15	447	59.0	117	1	HV12_MOUSE
16	446	58.9	117	1	HV52_MOUSE
17	445	58.8	117	1	HV13_MOUSE
18	444	58.7	117	1	HV14_MOUSE
19	441.5	58.3	118	1	HV51_MOUSE
20	415.5	54.9	143	1	HV1G_HUMAN
21	412	54.4	117	1	HV1G_HUMAN
22	398	52.6	117	1	HV1B_MOUSE
23	348	46.0	117	1	HV42_MOUSE
24	347.5	45.9	114	1	HV00_MOUSE
25	341.5	45.1	136	1	HV1E_MOUSE
26	341.5	45.1	119	1	HV16_MOUSE
27	339	44.8	142	1	HV01_RAT
28	335	44.3	117	1	HV41_MOUSE
29	333.5	44.1	119	1	HV37_MOUSE
30	331.5	43.8	146	1	HV21_MOUSE
31	327	43.2	118	1	HV32_MOUSE
32	325.5	42.1	121	1	HV40_MOUSE
33	319	42.0	121	1	HV3J_HUMAN
34	316	41.7	125	1	HV1E_HUMAN
35	312	41.2	117	1	HV1A_HUMAN
36	311.5	41.1	122	1	HV3G_HUMAN
37	308	40.7	115	1	HV32_MOUSE
38	306.5	40.5	126	1	HV3K_HUMAN
39	306	40.4	113	1	HV30_MOUSE
40	305.5	40.4	120	1	HV1H_HUMAN
41	304	40.2	116	1	HV3E_MOUSE
42	303.5	40.1	124	1	HV1D_HUMAN
43	302.5	40.0	111	1	HV35_MOUSE

ALIGNMENTS

44 301 39.8 123 1 HV25_MOUSE P01794 mus muscula
45 301 39.8 113 1 HV27_MOUSE P01796 mus muscula

```
RESULT 1
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751: P01752.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6;
RX MEDLINE: 81234548.
RA BOTTRELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
RL BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THE B1-8 MY CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL: J00529; G195115; -
DR PIR: A02034; MMS18.
DR HSSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT CHAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139
SQ SEQUENCE 139 AA; 15419 MW; DEB2C7DA CRC32;
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Query Match 79.2%; Score 599.5; DB 1; Length 139;
Best Local Similarity 80.7%; Pred. No. 2,4e-50;
Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

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QY 1 MWMSCITFLVSTFATSVHSQVOLOOPEAEVYKGTSTVYSS 60
DB 1 MWMSCITFLVSTFATSVHSQVOLOOPEAEVYKGTSTVYSS 60
QY 61 GQGLEWIGEIDPESNTNNTNOKFKKATLVYDISSSTAYVQSLSSDSAVYVCARGY 120
DB 61 GRGLEWIGRIDPNSGGKTKYKFKRSKATLVDPKPSSTAYVQSLSSDSAVYVCARGY 120
QY 121 DGMVDAIDYWGQGTSTVYSS 140
DB 121 YGSSY-FDYWGQGTTLTVSS 139
QY 121 YGSSY-FDYWGQGTTLTVSS 139
DB 121 YGSSY-FDYWGQGTTLTVSS 139
RESULT 2
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
```

OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84248078.
RA GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,
RA TUCKER P.W.,
RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).
DR HSP; A02033; HWS17.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION (TRPC 1017).
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; BEF6247B CRC32;

Query Match 73.8%; Score 559; DB 1; Length 138;
Best Local Similarity 75.9%; Pred. No. 1.7e-46;
Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVHSOVOLQOPGAEIVKPGASVOLSKSGHFTTNHIMHWKORP 60
QY 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR-G 119
DB 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCARSDG 120
QY 120 YDGDWDYADWGGGTSTVSS 140
DB 121 YDWD---FVWGGGTLTWFS 138

RESULT 3
HVO6_MOUSE STANDARD; PRT; 117 AA.
ID HVO6_MOUSE
AC P01750;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (102).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-G5BL/6;
RX MEDLINE; 81334548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.,
RL CELL. 24:625-637(1981).
CC -1- THIS GEMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR HSP; A02032; HWS02.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (102).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match 73.4%; Score 556; DB 1; Length 117;
Best Local Similarity 89.7%; Pred. No. 2.7e-46;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVHSOVOLQOPGAEIVKPGASVOLSKSGHFTTNHIMHWKORP 60
QY 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCA 116
DB 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCA 116

RESULT 4
HVL1_MOUSE STANDARD; PRT; 137 AA.
ID HVL1_MOUSE
AC P01755;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (S43).
OS MUS MUSCULUS (MUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81334548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.,
RL CELL. 24:625-637(1981).
CC -1- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NP8
CC ANTIBODIES).
DR EMBL; J00539; G195119; -.
DR PIR; A02038; G2MS43.
DR HSP; P01772; 1FGV.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;

Query Match 73.2%; Score 554.5; DB 1; Length 137;
Best Local Similarity 74.1%; Pred. No. 4.5e-46;
Matches 106; Conservative 9; Mismatches 19; Indels 9; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHSOVOLQOPGAEIVKPGTSYKLSCKGYFTSYMMHWKORP 60
DB 1 MGWSCIILFLVATATGVHSOVOLQOPGAEIVKPGASVOLSKSGHFTTNHIMHWKORP 60
QY 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR--- 118
DB 61 GGGLEWIGEIDPSNTNNOKEFGKATLVVDSSSTAYVQSLTSSEDSAVYYCAR 120
QY 118 GYDGDWDYADWGGGTSTVSS 140
DB 121 GRY-----EDYWGQGTTLTVSS 137
RESULT 5
HVO5_MOUSE

ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (3).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOWMELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
CC EMBL; J00536; G534035; -.
DR PIR; A02031; HYMS3.
DR HSSP; P01810; 1JHL.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (3).
FT DOMAIN 20 49 FRAMEWORK 1.
FT AC 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT FT 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 0F12FC8B CRC32;

Query Match 71.7%; Score 543; DB 1; Length 117;
Best Local Similarity 88.0%; Pred. No. 4.6e-45;
Matches 103; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
DB 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
QY 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCAR 117
DB 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCAR 117

RESULT 6
HV09_MOUSE STANDARD; PRT; 117 AA.
ID HV09_MOUSE P01753; P11271;
AC P01753; P11271;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOWMELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
RA BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
CC PIR; B02034; HYMS61.
DR HSSP; P01810; 1FVB.
KM IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (186-1).
FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT FT 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;

Query Match 70.9%; Score 537; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 1.7e-44;
Matches 99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
DB 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
QY 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCAR 117
DB 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCAR 117

RESULT 7
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE P01746;
AC P01746;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (9367).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE; 82152818.
RA SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
RA CAPRA J.D.;
RL SCIENCE 215:309-311(1982).
DR EMBL; J00493; G195007; -.
DR PIR; A02028; HYMS67.
DR HSSP; P01789; 6FAB.
KM IMMUNOGLOBULIN V REGION; ANTIBIOTIC ANTIBODY; HYBRIDOMA; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION (9367).
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;

Query Match 70.3%; Score 532; DB 1; Length 140;
Best Local Similarity 72.1%; Pred. No. 6.2e-44;
Matches 101; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
DB 1 MGWSCIIFLVSTATSVHSGVOVLOQPGAEIVKPGTSVKLSCKGYGTFTSYMMHWKORP 60
QY 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCARGY 120
DB 61 GQGLEWIGELIDPESNTNTNOKFKRATLVDISSTAYMQLSLTSEDSAVYYCARGY 120
QY 121 DGMDYADYWGQSTVYSS 140
DB 121 YGGSYDIDYWGQSTVYSS 140

RESULT 8
HV04_MOUSE STANDARD; PRT; 117 AA.
ID HV04_MOUSE P01748;
AC P01748;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (23).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
 RL CELL 24:625-637(1981).
 CC -1- THIS GERM-LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR PIR: A02030; HVMS23.
 DR HSP: P01810; JHHL.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (23).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12772 MW; 66B34D1A CRC32;

Query Match 69.6%; Score 527; DB 1; Length 117;
 Best Local Similarity 83.8%; Pred. No. 1.5e-43;
 Matches 98; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSOVQLOQPGALVYKPGTSVYKLSCKGYFTSYMMHWKORP 60
 DB 1 MGWSCIILFLVAAANGHSOVQLOQPGELVYKPGASVYKLSCKASGYFTSYMMHWKORP 60
 QY 61 GGGLEWIGELDPSESNYNOKFRKATLVVDISSSTAYMOLSTSEDSAVYYCAR 117
 DB 61 GGGLEWIGINIPNGNGTNNKFKSKVTLTVDKSSSTAYTQSLTSDSAVYYCAR 117

RESULT 9
 HVA9_MOUSE
 ID HY49_MOUSE STANDARD; PRT; 117 AA.
 AC P06328;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85099340.
 RA YANCOPOULOS G.D., ALT F.W.;
 RL CELL 40:271-281(1985).
 DR EMBL: M13788; G466292; -.
 DR PIR: A02035; MHMSB4.
 DR HSP: P01810; JHHL.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12834 MW; 85692FE5 CRC32;

Query Match 69.4%; Score 525; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 2.3e-43;
 Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSOVQLOQPGALVYKPGTSVYKLSCKGYFTSYMMHWKORP 60
 DB 1 MGWSCIILFLVAAANGHSOVQLOQPGELVYKPGASVYKLSCKASGYFTSYMMHWKORP 60
 QY 61 GGGLEWIGELDPSESNYNOKFRKATLVVDISSSTAYMOLSTSEDSAVYYCAR 117
 DB 61 GGGLEWIGINIPNGNGTNNKFKSKVTLTVDKSSSTAYTQSLTSDSAVYYCTR 117

RESULT 10
 HVA10_MOUSE
 ID HY10_MOUSE STANDARD; PRT; 117 AA.
 AC P01754; P11270;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (145).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
 RL CELL 24:625-637(1981).
 CC -1- THIS GERM-LINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 DR EMBL: J00533; G54033; -.
 DR PIR: C02034; HVMS45.
 DR HSP: P01810; JHHL.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (145).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12921 MW; D9EBB000 CRC32;

Query Match 68.6%; Score 519; DB 1; Length 117;
 Best Local Similarity 82.9%; Pred. No. 8.6e-43;
 Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSOVQLOQPGALVYKPGTSVYKLSCKGYFTSYMMHWKORP 60
 DB 1 MGWSCIILFLVAAANGHSOVQLOQPGELVYKPGASVYKLSCKASGYFTSYMMHWKORP 60
 QY 61 GGGLEWIGELDPSESNYNOKFRKATLVVDISSSTAYMOLSTSEDSAVYYCAR 117
 DB 61 GGGLEWIGRIDPNNGGTYNKKFKSKVTLTVDKSSSTAYMOLSTSEDSAVYYCAR 117

RESULT 11
 HVA15_MOUSE
 ID HY15_MOUSE STANDARD; PRT; 136 AA.
 AC P01759;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (BC11).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.

[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 82222262.
 RA KNAPP M.R., LIU C.-P., NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,
 BLATTNER F.R.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).
 DR EMBL; J00494; G195011; -.
 DR PIR; A02042; HVMSB1.
 DR HSSP; P01789; 1JEL.
 KM IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL
 FT CHAIN 1
 FT NON_TER 20 136 IG HEAVY CHAIN V REGION (BC11).
 FT SEQUENCE 136 AA; 15078 MW; E04F1C7F CRC32;

Query Match 65.7%; Score 497; DB 1; Length 136;
 Best Local Similarity 68.3%; Pred. No. 1.3e-40;
 Matches 97; Conservative 12; Mismatches 25; Indels 8; Gaps 2;

QY 1 MGMSCTILFVSTATSVHVOLOOQGAELVPGTSYKLSCKGYGTFSTYMMHWKORP 60
 DB 1 MGMSCTILFVSTATSVHVOLOOQGAELVPGTSYKLSCKGYGTFSTYMMHWKORP 60
 QY 61 GQGLEWIGELIDPSSESNYNOKFKGKATLVDISSTAYMOLSLTSEDSAVYYCAR--G 118
 DB 61 AKSLEWIGISTYNGNTSYNOKFKGKATLVDISSTAYMOLSLTSEDSAVYYCAR--G 120
 QY 119 GYDGDVAIDYWGQSTVYSS 140
 DB 121 NY-----FDYWGQSTVYSS 136

RESULT 12
 HV01_MOUSE STANDARD; PRT; 120 AA.
 AC P06329;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (AC38 15.3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RA MEDLINE; 84182519.
 RA DILDROP R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJEMSKY K.;
 RL EMBO J. 3:517-523(1984).
 DR PIR; A02037; MHMS15.
 DR HSSP; P01772; 1FQV.
 KM IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 98
 FT DOMAIN 99 105 V SEGMENT.
 FT DOMAIN 106 120 D SEGMENT.
 FT DISULFID 22 96 J SEGMENT.
 FT NON_TER 120 120 BY SIMILARITY.
 FT SEQUENCE 120 AA; 13311 MW; 85EC01BA CRC32;

Query Match 63.3%; Score 479.5; DB 1; Length 120;
 Best Local Similarity 75.2%; Pred. No. 5e-39;
 Matches 91; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 20 QVLOQPAELVPGTSYKLSCKGYGTFSTYMMHWKORPQGLEWIGELIDPSSESNYN 79
 DB 1 QVLOQPAELVPGTSYKLSCKGYGTFSTYMMHWKORPQGLEWIGELIDPSSESNYN 60
 QY 80 NOKFKGKATLVDISSTAYMOLSLTSEDSAVYYCARGDYVYDAIDYWGQSTVYSS 139
 DB 61 NEKFKGKATLVDISSTAYMOLSLTSEDSAVYYCARMDYEG--DRYDVGQSTVYSS 119
 QY 140 S 140

DB 120 S 120

RESULT 13
 HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 83131846.
 RA SIEKEVITZ M., GERTER M.L., BRODEUR P., RIBLET R.,
 MARSHAK-ROTHSTEIN A.;
 RL EUR. J. IMMUNOL. 12:1023-1032(1982).
 CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
 DR PIR; A02028; HVMSG7.
 DR HSSP; P01789; 6FAB.
 KM IMMUNOGLOBULIN V REGION; ANTIBODY; HYBRIDOMA.
 FT NON_TER 120 120
 FT SEQUENCE 120 AA; 13307 MW; BBACCA1 CRC32;

Query Match 61.8%; Score 468; DB 1; Length 120;
 Best Local Similarity 74.2%; Pred. No. 6.1e-38;
 Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 21 VQLOQPAELVPGTSYKLSCKGYGTFSTYMMHWKORPQGLEWIGELIDPSSESNYN 80
 DB 1 VQLOQPAELVPGTSYKLSCKGYGTFSTYMMHWKORPQGLEWIGELIDPSSESNYN 60
 QY 81 OKFKGKATLVDISSTAYMOLSLTSEDSAVYYCARGDYVYDAIDYWGQSTVYSS 140
 DB 61 EKFKGKATLVDISSTAYMOLSLTSEDSAVYYCARVYGGSYFDYWGQSTVYSS 120

RESULT 14
 HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (MPC 11).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 81053741.
 RA ZAKUT R., COHEN J., GIVOL D.;
 RL NUCLEIC ACIDS RES. 8:3591-3601(1980).
 RN [2]
 RP REVISIONS.
 RA ZAKUT R., COHEN J., GIVOL D.;
 RL NUCLEIC ACIDS RES. 8:4839-4840(1980).
 CC -1- THIS SEQUENCE WAS TRANSLATED FROM AN mRNA ISOLATED FROM A
 MYELOMA THAT SECRETES IGG2B.
 DR PIR; A02027; GYMS11.
 DR HSSP; P01810; 1MFE.
 KM IMMUNOGLOBULIN V REGION.
 FT NON_TER 121 121
 FT SEQUENCE 121 AA; 13135 MW; 2A8FC8CC CRC32;

DT 01-NOV-1998 (TEMBELREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TEMBELREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009516; E1311432; -.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SO SEQUENCE 81 AA; 9074 MW; 288593C4 CRC32;

Query Match 24.9%; Score 188.5; DB 2; Length 81;
 Best Local Similarity 40.5%; Pred. No. 1.5e-11;
 Matches 34; Conservative 20; Mismatches 25; Indels 5; Gaps 2;

QY 49 TSYMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSE 108
 DB 1 TSYMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSE 60
 QY 109 DSAVYICA--RGYDGMVDAIDYW 130
 DB 61 DTAIFYCARDRSGSNDW---LDPW 81

RESULT 7
 075726 PRELIMINARY; PRT; 77 AA.

ID 075726;
 AC 075726;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009523; E1311446; -.
 FT NON_TER 1 1
 FT NON_TER 77 77
 SO SEQUENCE 77 AA; 9022 MW; EB7B45BD CRC32;

Query Match 24.9%; Score 188.5; DB 2; Length 77;
 Best Local Similarity 40.0%; Pred. No. 1.4e-11;
 Matches 32; Conservative 20; Mismatches 25; Indels 3; Gaps 1;

QY 51 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 110
 DB 1 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 60
 QY 111 AVYYCARGYDGMVDAIDYW 130
 DB 61 AVYYCVR---DSYDGRGDFW 77

RESULT 8
 075730 PRELIMINARY; PRT; 78 AA.
 AC 075730;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009527; E1311454; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SO SEQUENCE 78 AA; 8994 MW; 0A38F0E5 CRC32;

Query Match 24.8%; Score 187.5; DB 2; Length 78;
 Best Local Similarity 42.1%; Pred. No. 1.8e-11;
 Matches 32; Conservative 18; Mismatches 23; Indels 3; Gaps 1;

QY 51 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 110
 DB 3 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 62
 QY 111 AVYYCAR---GYDGM 123
 DB 63 AVYHCARDVNGHFDYW 78

RESULT 9
 075728 PRELIMINARY; PRT; 77 AA.

ID 075728;
 AC 075728;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009525; E1311450; -.
 FT NON_TER 1 1
 FT NON_TER 77 77
 SO SEQUENCE 77 AA; 8925 MW; EA14CFDF CRC32;

Query Match 24.7%; Score 187; DB 2; Length 77;
 Best Local Similarity 41.6%; Pred. No. 1.9e-11;
 Matches 32; Conservative 20; Mismatches 21; Indels 4; Gaps 1;

QY 51 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 110
 DB 1 YMMHWKORPGQGLEWIGEDIPSESNNTYNQKFKGKATLVYDISSSTAYMQLSLTSEDS 60
 QY 111 AVYYCARG---GYDGM 123
 DB 61 AVYYCARGKRGSEFDYW 77

RESULT 10
 075734

ID 075734 PRELIMINARY; PRT; 81 AA.
AC 075734;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009531; E1311462; -.
FT NON_TER 1 81
FT SEQUENCE 81 AA; 9040 MW; 56B4D902 CRC32;
SQ

Query Match 24.5%; Score 185.5; DB 2; Length 81;
Best Local Similarity 42.0%; Pred. No. 2.9e-11;
Matches 34; Conservative 16; Mismatches 24; Indels 7; Gaps 1;

QY 50 SYMMVKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 109
DB 1 SYMMVKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 60
QY 110 SAVYYCAR-----GGYDGM 123
DB 61 TAVYYCARLVNKKYKPGMDVM 81
Db

RESULT 11
ID 075725 PRELIMINARY; PRT; 82 AA.
AC 075725;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009522; E1311444; -.
FT NON_TER 1 82
FT SEQUENCE 82 AA; 9566 MW; 1F2E1379 CRC32;
SQ

Query Match 24.1%; Score 182.5; DB 2; Length 82;
Best Local Similarity 45.1%; Pred. No. 5.7e-11;
Matches 37; Conservative 16; Mismatches 24; Indels 5; Gaps 4;

QY 51 YMMHWKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 110
DB 4 YMMHWKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 61
QY 111 AVYYCAR--GGYDGMVAIDYM 130
DB 62 AVYYCARPFGGKAMPY-FDIW 82
Db

RESULT 12
ID 075740 PRELIMINARY; PRT; 86 AA.
AC 075740;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009539; E1311474; -.
FT NON_TER 1 86
FT SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;
SQ

Query Match 23.9%; Score 181; DB 2; Length 86;
Best Local Similarity 48.5%; Pred. No. 8.3e-11;
Matches 32; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 52 WMHWKORPGGLEWGEIDPSE--SNTNNOFKGKATLTVDISSTAYMQLSLTSED 109
DB 3 WMHWKORPGGLEWGEIDPSE--SNTNNOFKGKATLTVDISSTAYMQLSLTSED 62
QY 110 SAVYYC 115
DB 63 TAVYYC 68
Db

RESULT 13
ID 075744 PRELIMINARY; PRT; 74 AA.
AC 075744;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AJ009545; E1311484; -.
FT NON_TER 1 74
FT SEQUENCE 74 AA; 8541 MW; 46693A8A CRC32;
SQ

Query Match 23.9%; Score 181; DB 2; Length 74;
Best Local Similarity 40.5%; Pred. No. 7.1e-11;
Matches 32; Conservative 14; Mismatches 27; Indels 6; Gaps 1;

QY 52 WMHWKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 111
DB 2 WMHWKORPGGLEWGEIDPSESNTNNOFKGKATLTVDISSTAYMQLSLTSED 61
QY 112 VYICARGYDGMVAIDYM 130
Db

Db 62 VYYCATG-----FALDLW 74

RESULT 14
075722

ID	075723	PRELIMINARY;	PRT;	78	AA.
32	075723				

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLEL, 08, LAST ANNOTATION UPDATE)

20 MINUTE CHINA PROTECTED SECTION (TANPOUNEN) /
GN VH.

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CS HOMO SAPIENS (HUMAN);

CC PRIMATES; CATARRHINI; HOMINIDAE; HOMO,
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE;

RA FISCHER M., KOEPPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry he

RT mutated VH region genes.";
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR	EMBL; AJ009520; E1311440; -.
NON TER	1
FT	1

ET	NON_TER	78	78
SO	SEQUENCE	78 AA.	9075 MW. DEEDD569 CBC32.

Query Match	23.68;	Score 179;	DB 2;	Length 78;
Post Test Classification	40.28;	Post Test Score	179.00;	Post Test Length 78.00;

Matches 31; Conservative 13; Mismatches 19; Indels 0

QY 55 WVKRPGGLEWIGEIDPSESNTNYNOKFKKATLTVDISSSTAYMQLSLTSEDS

Db 1 WVRQAPGKGLWVXKRISDESRIN^YADSVKGRFTISRDNAKNTLYLQ^YMNSLR^YAE^YDT^Y

QY 115 CAR 117

Db 61 CAR 63

RESULT 15
075722

AC	075722:	PRELIMINARY;	86 AA.
ID	0/5/22	PRT;	

DT	01-NOV-1998	(TREMBLREL, 08, CREATED)
DT	01-NOV-1998	(TREMBLREL, 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (EPACMENT)

GN
VH.
HOW CAPTAINS (HUMAN)

OC EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
MAMMALS; CARNIVORA; ROSSIDAE

RN [1]

RC TISSUE-INTESTINE;

RT "Human IgA and IgM secreting intestinal plasma cells carry he

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DN	EMBL; AC009319; E1511430; -
FT	NON_TER 1 1

F1	NON_TER	86	86
SQ	SEQUENCE	86 AA;	9769 MW; 5F6AC773 CRC32;

Query Match	23.5%;	Score 1/8;	DB 2;	Length 86;
Best Local Similarity	41.28;	Pred. No. 1.6e-10;		

Matches 35; Conservative 17; Mismatches 29; Indels 4

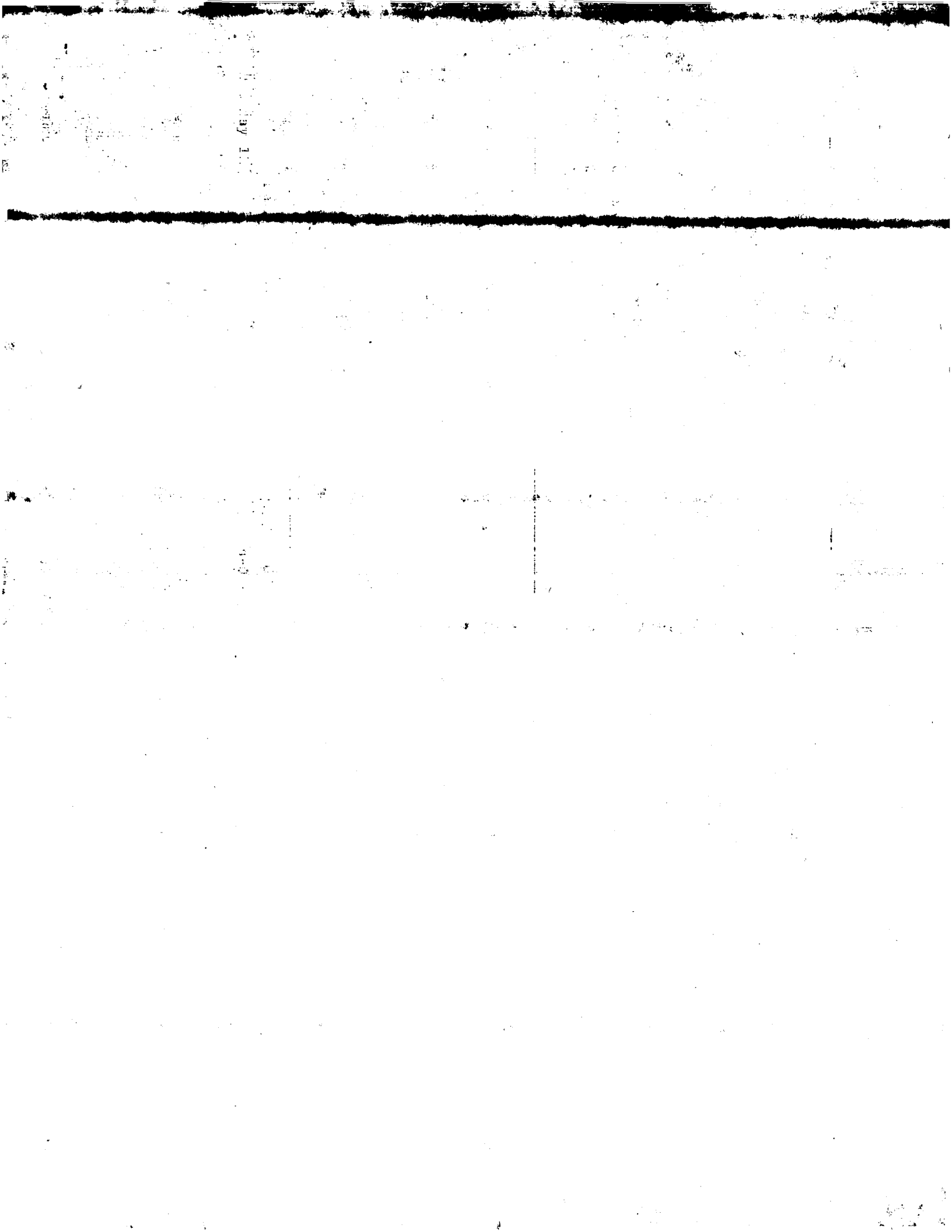
QY 50 SYMMHWKQRPGGLEWIGEIDPSESNTNYNQKFKGATLTVDISSSTAYMQLSSH

Db 2 SHNMKWVROAPGKGLEWVASISGSGVYIYYGESVKGRTVSRDNAKNSLYLEMDLDED 61

QY 110 SAVYCA--RGGYDGWD--YAI DYW 130

Db 62 TAVYYCARDRGAACTDYQYGM⁺DVW 86

Search completed: May 11, 1999, 12:21:01
Job time: 253 sec



GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 1999, 12:14:53 ; Search time 44.09 seconds
(without alignments)
64.222 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGMWDYALDYGQGTSTVYSS 140

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database: A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	757	100.0	140	1	Murine Act-1 heavy
2	730	96.4	137	1	Protein sequence o
3	713	94.2	144	1	Consensus protein
4	632	83.5	180	1	Heavy chain of a h
5	597	78.9	464	1	MAB 55.1 heavy cha
6	594.5	78.5	443	1	Single chain anti
7	589	77.8	140	1	VH425 antibody c10
8	586	77.4	136	1	Sequence encoded b
9	586	77.4	136	1	Chimeric anti-hepa
10	586	77.4	136	1	Mouse-human chime
11	586	77.4	136	1	Anti-hepatitis B h
12	586	77.4	136	1	Human anti-hepatit
13	586	77.4	136	1	Human anti-hepatit
14	586	77.4	136	1	Human anti-hepatit
15	583	77.0	143	1	MAB SCH94.03 heavy
16	551.5	72.9	144	1	Heavy chain variab
17	551.5	72.9	143	1	Mouse MAB 2E12 H C
18	549	72.5	138	1	Amino acid sequenc
19	548.5	72.5	137	1	Monoclonal antibod
20	545	72.0	140	1	Murine variable re
21	544.5	71.9	139	1	p64-h2 protein pro
22	543	71.7	140	1	MAB Co-1 heavy cha
23	538	71.1	119	1	Anti-DNA antibody
24	537	70.9	140	1	Co-1 Heavy Chain V
25	536.5	70.9	145	1	Anti-tobacco mosai
26	536	70.8	119	1	Anti-EGFR antibody
27	532	70.3	138	1	Murine ICR-1.1 V-H
28	532	70.3	138	1	Murine antibody IC
29	531	70.1	136	1	Sequence of the he
30	529.5	69.9	159	1	Heavy chain of mon
31	528.5	69.8	139	1	Anti-HMG MAB CTMO
32	525.5	69.4	428	1	Single chain anti
33	521.5	68.9	139	1	CTMO1 VH. Anti-hum
34	521.5	68.9	269	1	PRAS11 between HI
35	521.5	68.9	435	1	scfv PRAS108 and p
36	521.5	68.9	402	1	scfv PRAS110 and p
37	521.5	68.9	269	1	scfv PRAS107 and p
38	520.5	68.8	122	1	B-cell lymphoma CH
39	520	68.7	445	1	MAB 55.1 heavy cha
40	520	68.7	119	1	Anti-EGFR antibody
41	518.5	68.5	118	1	Murine antibody he
42	516.5	68.2	141	1	M4 Heavy Chain V
43	516.5	68.2	120	1	M4 Heavy anti-CD18 A

ALIGNMENTS

44 516.5 68.2 141 1 W05216 MAB ME4 heavy chain
45 516.5 68.2 464 1 W14941 3F4 Human IgG4 exp

RESULT 1
ID W53815
AC W53815
DE 14-JUL-1998 (first entry)
KW Murine Act-1 heavy chain variable region.
KW Mouse: Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MacdCM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW inflammatory bowel disease.
OS Mus sp.
FH Key
FT Peptide 1..19 Location/Qualifiers
FT Protein /note="signal peptide"
FT Protein /note="mature protein"
PN W09806248-A2.
PD 19-FEB-1998.
PF 06-AUG-1997; U13884.
PR 15-AUG-1996; US-700737.
PA (LEUK-) LENDROSITE INC.
PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
PI Saldanha J;
DR WPI: 98-159172/14.
DR N-PSDB: V20078.
PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
PT used for treating inflammatory disease, pancreatitis, diabetes,
PT asthma, graft versus host disease and sarcoidosis
PS Claim 27; Fig 9; 145pp; English.
CC The present sequence represents the heavy chain variable region of
CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
CC integrin. Muscosal adressin cell adhesion molecule-1 (MacdCM-1) is a
CC ligand of this particular integrin. The Act-1 antibody interferes with
CC endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
CC leukocyte infiltration of tissues, e.g. for treating inflammatory
CC diseases such as inflammatory bowel disease. The immunoglobulin can
CC also be used for detection, isolation and diagnosis.
SQ Sequence 140 AA;

Query Match 100.0%; Score 757; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 6.9e-54;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVOLOQPEAEVYKGTSTVYSSHWYKORP 60
DB 1 MGWSCIILFLVSTATSVHSQVOLOQPEAEVYKGTSTVYSSHWYKORP 60
QY 61 GGGLEWIGEIDPESNTNNTNOKFKRATLTVDISSSTAYWQLSLSEDSAVYYCARGGY 120
DB 61 GGGLEWIGEIDPESNTNNTNOKFKRATLTVDISSSTAYWQLSLSEDSAVYYCARGGY 120
QY 121 DGMWDYALDYGQGTSTVYSS 140
DB 121 DGMWDYALDYGQGTSTVYSS 140

RESULT 2
ID W53818
AC W53818;
DE 14-JUL-1998 (first entry)

DE Protein sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW Inflammatory bowel disease.
 OS Mus sp.
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSTE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20089.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 2; 145pp; English.
 CC The present sequence represents the amino acid sequence comprising the
 CC variable region of murine Act-1 antibody determined from clone H2B#34.
 CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin
 CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
 CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
 CC to MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. The present sequence was used to construct chimeric,
 CC humanised Act-1 antibodies, which contain murine antigen binding regions.
 CC The humanised immunoglobulin can be used to inhibit the interaction of
 CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
 CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
 CC treating inflammatory diseases such as inflammatory bowel disease. The
 CC immunoglobulin can also be used for detection, isolation and diagnosis.
 SQ Sequence 137 AA;

Query Match 96.4%; Score 730; DB 1; Length 137;
 Best Local Similarity 98.5%; Pred. No. 9.6e-52;
 Matches 135; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWCIILFLVSTATSVHSOVQLOPGAEIVKPGSVKLSCKGYGTFTSYMMHWKORP 60
 DB 1 MGWYIILFLVSTATSVHSOVQLOPGAEIVKPGSVKLSCKGYGTFTSYMMHWKORP 60
 QY 61 GGGLEWIGIDPESNTNMYNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGGY 120
 DB 61 GGGLEWIGIDPESNTNMYNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGGY 120
 QY 121 DGMIDYDAIDYWGQGTSTVTS 137
 DB 121 DGMIDYDAIDYWGQGTSTVTS 137

RESULT 3
 W53816
 ID W53816 standard; Protein; 144 AA.
 AC W53816;
 DT 14-JUL-1998 (first entry)
 DE Consensus protein sequence of the murine variable heavy chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW Inflammatory bowel disease.
 OS Mus sp.
 PN Mus sp.
 FH Key
 FT MISC_difference 2 location/Qualifiers
 FT MISC_difference 3 /note- "not specified, encoded by RRA"
 FT MISC_difference 4 /note- "not specified, encoded by TGS"
 FT MISC_difference 5 /note- "not specified, encoded by ASC"

FT FT /note- "not specified, encoded by TRK"
 FT MISC_difference 6 /note- "not specified, encoded by RNC"
 FT MISC_difference 7 /note- "encoded by ATY"
 FT MISC_difference 8 /note- "not specified, encoded by YNC"
 FT Peptide 1.19
 FT Protein /note- "signal peptide"
 FT /note- 20.144
 FT /note- "mature protein"
 FT Region 20.49
 FT /note- "framework region 1"
 FT /note- 50.54
 FT /note- "CDR1"
 FT Region 55.68
 FT /note- "framework region 2"
 FT Region 69.85
 FT /note- "CDR2"
 FT Region 86.117
 FT /note- "framework region 3"
 FT Region 118.130
 FT /note- "CDR3"
 FT Region 131.141
 FT /note- "framework region 4"
 PN WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSTE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI: 98-159172/14.
 DR N-PSDB: V20085.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 1; 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 144 AA;

Query Match 94.2%; Score 713; DB 1; Length 144;
 Best Local Similarity 99.3%; Pred. No. 2.3e-50;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ILFLVSTATSVHSOVQLOPGAEIVKPGSVKLSCKGYGTFTSYMMHWKORPGGLEW 66
 DB 7 IFLVSTATSVHSOVQLOPGAEIVKPGSVKLSCKGYGTFTSYMMHWKORPGGLEW 66
 QY 67 IGEIDPESNTNMYNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGGYDMDYA 126
 DB 67 IGEIDPESNTNMYNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGGYDMDYA 126
 QY 127 IDWVGQGTSTVTS 140
 DB 127 IDWVGQGTSTVTS 140

Db 127 IDYWGCGTSTVYSS 140

RESULT 4

W53813

ID W53813 standard; Protein: 180 AA.

AC W53813;

DE Heavy chain of a humanised murine Act-1 antibody.

KM Mouse: Act-1 antibody; human alpha4-beta7 integrin;

KM Muscosa addressin cell adhesion molecule-1; MadCAM-1;

KM humanised antibody; murine antigen binding region; inhibition;

KM leucocyte infiltration of tissue; treatment; inflammatory disease;

KM inflammatory bowel disease.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

OS Key

FT Peptide

FT 1..19

FT /note="signal peptide"

FT 20..180

FT /note="mature protein"

PN W09806248-A2.

PD 19-FEB-1998.

PF 06-AUG-1997; 013884.

PR 15-AUG-1996; 05-700737.

PA (LEUK-) LEUKOSITE INC.

PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,

PI Saldanha J.

DR WPI: 98-159172/14.

DR N-PSDB: V20076.

PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -

PT used for treating inflammatory disease, pancreatitis, diabetes,

PS asthma, graft versus host disease and sarcoidosis

PS Claim 20: Fig 11; 145pp; English.

CC The present sequence represents the heavy chain of humanised murine

CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.

CC Muscosa addressin cell adhesion molecule-1 (MadCAM-1) is a ligand of

CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7

CC integrin binding to MadCAM-1, which is present of high endothelial

CC venules in mucosal lymph nodes. The humanised immunoglobulin can be

CC used to inhibit the interaction of cells bearing alpha4-beta7 with

CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting

CC leucocyte infiltration of tissues, e.g. for treating inflammatory

CC diseases such as inflammatory bowel disease. The immunoglobulin can

CC also be used for detection, isolation and diagnosis.

CC Sequence 180 AA;

SQ

Query Match

Best Local Similarity 85.9%; Score 632; DB 1; Length 180;

Matches 116; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFVSTATSVHSQVLOQPGAEVLRKGTGKSGYGTFTSYMMHWKORPGGGL 65

DB 6 VILFVSTATSVHSQVLOQPGAEVLRKGTGKSGYGTFTSYMMHWKORPGGRL 65

QY 66 WIEIDPSESTNTYNQKFKRATLTVDISSSTAYMQSLTSESAVYYCARGGYDWDY 125

DB 66 WIEIDPSESTNTYNQKFKRATLTVDISSSTAYMQSLTSESAVYYCARGGYDWDY 125

QY 126 AIDYWGCGTSTVYSS 140

DB 126 AIDYWGCGTSTVYSS 140

RESULT 5

R76088

ID R76088 standard; Protein: 464 AA.

AC R76088;

DT 21-NOV-1995 (first entry)

DE MAb 55.1 heavy chain.

KW Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;

KW transgenic animal; transgenic plant; antibody engineering;

KW humanized antibody; immunotoxin.

OS Mus sp.

OS Key

FT Peptide

FT 1..19

FT /label="Sig_peptide"

FT 20..464

FT /label="Mat_protein"

FT /note="claim 3, page 97-98"

PN W09515382-A.

PD 08-JUN-1995.

PF 29-NOV-1994; G02610.

PR 03-DEC-1993; GB-024819.

PR 03-JUN-1994; GB-011089.

PA (ZENE) ZENCA LTD.

PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;

PI Rose MS, Wright AF;

DR WPI: 95-215262/28.

DR N-PSDB: 094037.

PT Antigen binding structures containing CDRs recognising the CA55.1

PT antigen - produced by hybridomas and host cells, for use in the

PS diagnosis and therapy of cancer

PS disclosure; Fig.15; 121pp; English.

CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated

CC antigen CA55.1. cDNAs for the heavy (094037) and light (094036)

CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scv or

CC v-mim humanized 55.1 constructs have been expressed in myeloma

CC cells and E. coli.

CC Sequence 464 AA;

SQ

Query Match

Best Local Similarity 78.9%; Score 597; DB 1; Length 464;

Matches 112; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGNSCIILFVSTATSVHSQVLOQPGAEVLRKGTGKSGYGTFTSYMMHWKORP 60

DB 1 MGNSCIILFVSTATSVHSQVLOQPGAEVLRKGTGKSGYGTFTSYMMHWKORP 60

QY 61 GGGLEWIGETIDPESNTNTYNQKFKRATLTVDISSSTAYMQSLTSESAVYYCARGY 120

DB 61 GGGLEWIGETIDPESNTNTYNQKFKRATLTVDISSSTAYMQSLTSESAVYYCARGY 120

QY 121 DGYDADYDWGCGTSTVYSS 140

DB 121 YGYDADYDWGCGTSTVYSS 140

RESULT 6

W24025

ID W24025 standard; Protein: 443 AA.

AC W24025;

DT 04-MAR-1998 (first entry)

DE Single chain antigen hybrid receptor.

KW Hybrid receptor; single chain antigen; gene therapy; diagnosis;

KW signal conduction; receptor; control region.

OS Synthetic.

OS Homo sapiens.

OS Key

FT Peptide

FT 1..19

FT /label="leader_peptide"

FT 20..444

FT /note="single chain antigen hybrid receptor"

FT 20..139

FT /label="VH_B_1-8"

FT 140..154

FT /note="variable heavy chain region of BI-8 antibody"

FT /label="(Gly_Ser)3"

FT /note="linker region"

FT 155..264

FT /label="VL_B_1-8"

FT Region /note="variable light chain region of B1-8 antibody"
 FT 265..309
 FT /label=CD_8-alpha_hinge
 FT Domain 310..330
 FT /label=transmembrane_domain
 FT 331..444
 FT /label=cytoplasmic_domain
 PN WO9720938-A2.
 PD 12-JUN-1997.
 PF 03-DEC-1996; D02334.
 PR 05-DEC-1995; DE-045351.
 PA (HYPR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
 PI KULMBURG P, Mettelmann R, Rosenthal F;
 DR N-PSDB; T77137.
 DR WPI; 97-319784/29.
 PT Cells with hybrid receptor having extracellular and intracellular
 PT regions of different origins - useful in gene therapy and diagnosis
 PT of tumours
 PS Example 3; Fig 4; 46pp; German.
 CC This sequence represents a novel single chain antigen hybrid receptor
 CC (HR) and contains an extracellular domain specific for the hapten
 CC 4-hydroxy-5-iodo-3-nitrophenyl acetate (NIP) coupled to the CD8-alpha
 CC region and the transmembrane and signal-conducting intracellular parts
 CC of the CD3-zeta molecule. Such hybrid receptors comprise a receptor part
 CC localised on the outside of the cell and specific to a particular signal
 CC molecule and a receptor part originating from another receptor, localised
 CC on the inside of the cell and capable of setting off a signal inside the
 CC cell. The cell should also contain at least one other gene construct with
 CC a control region which can interact with the signal sent out by the
 CC hybrid receptor and thereby control expression of a transgene bound to
 CC this control region. Such cells are useful in gene therapy or for
 CC diagnostic purposes.
 SQ Sequence 443 AA;

Query Match 78.5%; Score 594.5; DB 1; Length 443;
 Best Local Similarity 80.7%; Pred. No. 1.9e-40;
 Matches 113; Conservative 6; Mismatches 20; Indels 1; Gaps 1;

QY 1 MGNSCILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSYMMHWKQRP 60
 DB 1 MGNSCILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSYMMHWKQRP 60
 QY 61 GGGLEWIGEIDPSESNNTNQNKKFKATLVYDISSSTAYVQLSSLSSEDSAVYYCARGY 120
 DB 61 GGGLEWIGEIDPSESNNTNQNKKFKATLVYDISSSTAYVQLSSLSSEDSAVYYCARGY 120
 QY 121 DGMDYALDYWGQGTSTVYSS 140
 DB 121 YGSSY-PDYWGQGTSTVYSS 139

RESULT 7
 ID R27049 standard; Protein; 140 AA.
 AC R27049;
 DT 01-MAR-1993 (first entry)
 DE VH425 antibody cloned into pUC18.
 KM Monoclonal antibody; complementarity determining region; framework;
 KM antigens; tumour; melanoma; carcinoma; glioma; light; heavy;
 KW variable; chain.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT 1..19
 FT /note="signal peptide"
 FT 20..140
 FT /note="mature protein"
 FT 50..54
 FT /label=CDR1
 FT 69..85
 FT /label=CDR2
 FT 118..129
 FT /label=CDR3

PN WO9215683-A.
 PD 17-SEP-1992.
 PF 04-MAR-1992; E00480.
 PR 06-MAR-1991; EP-103389.
 PA (MERE) MERCK PATENT GMBH.
 PI Bendig MM, Kettleborough CA, Saldanha J;
 DR WPI; 92-331729/40.
 DR N-PSDB; Q28739.
 PT Human monoclonal antibodies binding to human receptors - for
 PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma
 PS Disclosure; Fig 2; 89pp; English.
 CC The variable heavy chain of monoclonal antibody 425 was prep'd. from
 CC a synthetic cDNA sequence in which mutations had been made to the 5'
 CC and 3' ends to allow for cloning into HCWV expression vectors.
 CC Donor splice sites were recreated in the 3' flanking regions to
 CC allow correct splicing of the variable and constant regions. The
 CC 5' sequence was altered to introduce an initiation codon.
 CC The cloned antibody may be used int the prodn. of reshaped or
 CC humanised antibodies which are less immunogenic than native
 CC antibodies and may be used to combat e.g. glioma, melanoma or
 CC carcinoma.
 SQ See also R27299-300 and R27037-41.
 SQ Sequence 140 AA;

Query Match 77.8%; Score 589; DB 1; Length 140;
 Best Local Similarity 80.7%; Pred. No. 1.6e-40;
 Matches 113; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 1 MGNSCILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSYMMHWKQRP 60
 DB 1 MGNSCILFLVSTATSVHSQVLOQPGAEIVKPGTSVKLSCKGYGFTSYMMHWKQRP 60
 QY 61 GGGLEWIGEIDPSESNNTNQNKKFKATLVYDISSSTAYVQLSSLSSEDSAVYYCARGY 120
 DB 61 GGGLEWIGEIDPSESNNTNQNKKFKATLVYDISSSTAYVQLSSLSSEDSAVYYCARGY 120
 QY 121 DGMDYALDYWGQGTSTVYSS 140
 DB 121 DYDGRFYDYWGQGTSTVYSS 140

RESULT 8
 ID P70624 standard; Protein; 136 AA.
 AC P70624;
 DT 09-APR-1991 (first entry)
 DE Sequence encoded by anti-hepatitis B heavy chain variable region in
 DE pING2006E.
 KW Chimeric antibody; Anti-cancer antibody.
 PN WO8702671-A.
 PD 07-MAY-1987.
 PF 27-OCT-1986; U02269.
 PR 01-NOV-1985; US-793980.
 PA (ITGE-) INT GENETIC ENG INC.
 PA (ROBL/) ROBINSON R R.
 PI Robinson RR, Liu AY, Horwitz AH, Wall R;
 DR N-PSDB; N70967, N70968.
 DR WPI; 87-136004/19.
 PT Prodn. of immunoglobulin chains and molecules - is by recombinant
 PT DNA procedures, with chimeric antibodies etc. related to cancer
 PT specific antigens.
 PS Example; Fig 12B; 126pp; English.
 CC The patentors claim a chimeric antibody molecule comprising 2 light
 CC chains and 2 heavy chains, each comprising a constant human region
 CC and a variable non-human region. Coding sequences for the Ig chains
 CC are also claimed. The invention provides consensus sequences of
 CC light and heavy chain J regions useful in the design of
 CC oligonucleotides (UTGs) for use as primers or probes for cloning
 CC immunoglobulinlight or heavy chain mRNAs or genes. Depending on the
 CC nature of design of a particular UTG, it may be capable of
 CC hybridizing to all Ig mRNAs or genes containing a single specific J
 CC sequence. UTG denotes universal immunoglobulin gene.
 SQ Sequence 136 AA;


```

Db      1  MGMSYILFLVATADVHSQVLOOPGAEIVKPGASVYVSCASGYFTSTWMMHWKORP 60
QY      61  GGGLEWIGEIDPSSNTYNNKFKKATLTVDISSSTAYMOLSLTSDSAVYYCARGGY 120
Db      61  GGGIDWIGEINPSNGRTYNNKFKKATLTVDKSSSTAYMOLSLTSDSAVYYCASYDY 120
QY      121  DGMDYDAIDYMGQGTSTVSS 140
Db      121  D-W---FAYMGQGLTYTVSS 136

RESULT  11
W10584
ID W10584 standard; Protein; 136 AA.
AC W10584;
DE Anti-hepatitis B heavy chain variable region.
KW Immunoglobulin G; IgG; heavy chain; recombinant production;
KW antibody; passive immunisation; serum sickness; anaphylactic shock;
KW immunosassay; imaging; reagent; complement mediated lysis;
KW therapy; hepatitis B virus; variable region; HBV.
OS Mus spp.
PN US5595898-A.
PD 21-JAN-1997.
PF 01-NOV-1985; 793980.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PA (XOMA ) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 97-107579/10.
DR N-PSDB; T36303, T36304.
PT Nucleic acid encoding immunoglobulin fragment - comprising
PT dicistronic transcription unit with pectate lyase signal sequences
PS Example; Fig 12B; 98pp; English.
CC The cDNA sequence encoding present anti-hepatitis B heavy chain
CC variable sequence, was used in the preparation of a novel
CC polynucleotide molecule encoding an Ig fragment. The DNA
CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC secretion signal sequences respectively linked to a DNA sequence
CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC single prokaryotic promoter so as to form a dicistronic
CC transcription unit, provided that the Ig fragment can bind an
CC antigen and is produced and secreted by an E. coli host cell when
CC the nucleic acid molecule is expressed in the host cell.
CC The polynucleotide molecule is used for the production of
CC recombinant antibodies, which can be used for passive immunisation
CC without negative immune reactions (e.g. serum sickness and
CC anaphylactic shock), in labelled forms as immunoassay or imaging
CC reagents, in complement mediated lysis and for therapeutic
CC purposes when coupled to a toxin or other therapeutic agent.
SQ Sequence 136 AA;

```

Query Match 77.4%; Score 586; DB 1; Length 136;
 Best Local Similarity 81.4%; Pred. No. 2.8e-40;
 Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

```

QY      1  MGMSYILFLVATADVHSQVLOOPGAEIVKPGASVYVSCASGYFTSTWMMHWKORP 60
Db      1  MGMSYILFLVATADVHSQVLOOPGAEIVKPGASVYVSCASGYFTSTWMMHWKORP 60
QY      61  GGGLEWIGEIDPSSNTYNNKFKKATLTVDISSSTAYMOLSLTSDSAVYYCARGGY 120
Db      61  GGGIDWIGEINPSNGRTYNNKFKKATLTVDKSSSTAYMOLSLTSDSAVYYCASYDY 120
QY      121  DGMDYDAIDYMGQGTSTVSS 140

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Db      121  D-W---FAYMGQGLTYTVSS 136

RESULT  12
W47510
ID W47510 standard; Protein; 136 AA.
AC W47510;
DE Anti-hepatitis B heavy chain.
KW Human anti-hepatitis antibody heavy chain.
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
OS Homo sapiens.
PN US5698435-A.
PD 16-DEC-1997.
PF 06-JUN-1995; 467140.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 06-JUN-1995; US-467140.
PA (XOMA ) XOMA CORP.
PI Better M. Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 98-051492/05.
DR N-PSDB; V18553, V18554.
PT DNA encoding secreted immunoglobulin fragments - comprising at
PT least the variable regions of light or heavy chains
PS Example II; Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody L6 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 136 AA;

```

Query Match 77.4%; Score 586; DB 1; Length 136;
 Best Local Similarity 81.4%; Pred. No. 2.8e-40;
 Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

```

QY      1  MGMSYILFLVATADVHSQVLOOPGAEIVKPGASVYVSCASGYFTSTWMMHWKORP 60
Db      1  MGMSYILFLVATADVHSQVLOOPGAEIVKPGASVYVSCASGYFTSTWMMHWKORP 60
QY      61  GGGLEWIGEIDPSSNTYNNKFKKATLTVDISSSTAYMOLSLTSDSAVYYCARGGY 120
Db      61  GGGIDWIGEINPSNGRTYNNKFKKATLTVDKSSSTAYMOLSLTSDSAVYYCASYDY 120
QY      121  DGMDYDAIDYMGQGTSTVSS 140

```

DB 121 D-W---FAYWGGTWTAVSS 136

RESULT 13

W41054
ID W41054 standard; Protein: 136 AA.
AC W41054;
DE 01-JUN-1998 (first entry)
KW Human anti-hepatitis antibody heavy chain.
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
OS Homo sapiens.
PN US5693493-A.
PD 02-DEC-1997.
PF 25-MAY-1995; 450731.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PA (XOMA) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 98-031749/03.
DR N-PSDB: V03836, V03866.
PT Production of chimeric antibody fragments - by culturing E. coli
PT transformed with dicistronic expression cassette
PS Example II: Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody L6 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 1; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.8e-40;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGMSCTILFLVSTATSVHSVOVLOQPGAEIYVKGTSYKLSCKGYGTFSTYMMHWKORP 60
DB 1 MGMSCTILFLVATARVHSVOVLOQPGAEIYVKGTSYKLSCKGYGTFSTYMMHWKORP 60
QY 61 GGGLMEIGELIDSESNNTNOKFKKATITVDISSSTAYMQLSLTSEDSAYYYCARGGY 120
DB 61 GGGLDWIGELINPNSNGRTNNEKFKSKATITVDSSSTAYMQLSLTSEDSAYYYCASDYD 120
QY 121 DGWDYALDWGQGTSTVSS 140

DB 121 D-W---FAYWGGTWTAVSS 136

RESULT 14

W47517
ID W47517 standard; Protein: 136 AA.
AC W47517;
DE 05-JUN-1998 (first entry)
KW Human anti-hepatitis antibody heavy chain.
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
OS Homo sapiens.
PN US5698417-A.
PD 16-DEC-1997.
PF 06-JUN-1995; 466203.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PA (XOMA) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL;
DR WPI: 98-031487/05.
DR N-PSDB: V18589, V18590.
PT Production of recombinant immunoglobulin fragment - comprising Fd
PT molecule and light chain
PS Example II: Fig 12B; 98pp; English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody L6 raised
CC against human lung carcinoma cells. The invention provides a novel
CC approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 1; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.8e-40;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGMSCTILFLVSTATSVHSVOVLOQPGAEIYVKGTSYKLSCKGYGTFSTYMMHWKORP 60
DB 1 MGMSCTILFLVATARVHSVOVLOQPGAEIYVKGTSYKLSCKGYGTFSTYMMHWKORP 60
QY 61 GGGLMEIGELIDSESNNTNOKFKKATITVDISSSTAYMQLSLTSEDSAYYYCARGGY 120
DB 61 GGGLDWIGELINPNSNGRTNNEKFKSKATITVDSSSTAYMQLSLTSEDSAYYYCASDYD 120

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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:00:29 ; Search time 962.98 Seconds

(without alignments)
2006.143 Million cell updates/sec

Title: US-08-700-737-18

Perfect score: 540
Sequence: 1 ATGAATGCACCTGGGTGAT.....CCGACCGGTGACGGTGTCTCG 540

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database :

GenEmbl.*
1: gb_dal.*
2: gb_ba2.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl1.*
9: gb_pl2.*
10: gb_pr1.*
11: gb_pr2.*
12: gb_pr3.*
13: gb_ro.*
14: gb_st.*
15: gb_sy.*
16: gb_un.*
17: gb_vl.*
18: gb_htg.*
19: em_ba.*
20: em_fun.*
21: em_hum1.*
22: em_hum2.*
23: em_in.*
24: em_om.*
25: em_or.*
26: em_ov.*
27: em_pat.*
28: em_ph.*
29: em_pl.*
30: em_ro.*
31: em_sy.*
32: em_un.*
33: em_vl.*
34: em_htg.*
35: em_st.*
36: gb_ba1.*
37: gb_ba2.*
38: gb_pl1.*
39: gb_pl2.*
40: gb_pr1.*
41: gb_pr2.*
42: gb_pr3.*
43: gb_sts.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description

1	354.4	65.6	9209	6	AR000007	AR000007 Sequence
2	354.4	65.6	9209	6	AR015961	AR015961 Sequence
3	329.4	61.0	1572	6	A44967	A44967 Sequence 23
4	329.4	61.0	1572	6	I64458	I64458 Sequence 23
5	327.8	60.7	762	6	I69485	I69485 Sequence 57
6	327.8	60.7	762	6	I73104	I73104 Sequence 57
7	327.8	60.7	762	6	I79289	I79289 Sequence 57
8	327.8	60.7	762	6	I87063	I87063 Sequence 57
9	326.2	60.4	531	10	HDWIGHDJA	L23555 Human IGH C
10	324.8	60.1	1544	13	MUSIGBIHL	L23555 Human IGH C
11	321.6	59.6	1599	10	HDWIGHDJA	D14625 Mouse mRNA
12	321.6	59.6	1599	10	HDWIGHDJA	M87789 Human (hybr
13	318.4	59.0	3282	6	I58596	I58596 Sequence 15
14	318.4	59.0	13254	6	I58596	I58596 Sequence 15
15	318.4	59.0	3282	6	I58609	I58609 Sequence 16
16	318.4	59.0	13254	6	I58610	I58610 Sequence 17
17	317.2	58.7	530	10	HSU43758	U43758 Human Immun
18	317.2	58.7	530	10	HSU43758	U43758 Human Immun
19	317.2	58.7	533	10	HSU43762	U43762 Human Immun
20	317	58.7	533	10	HSU43762	U43762 Human Immun
21	317	58.7	536	10	HS20166	U43752 H.sapiens m
22	308.8	57.2	516	10	HS20166	U43752 H.sapiens m
23	308.8	57.2	516	10	HS20166	U43752 H.sapiens m
24	306	56.7	522	10	HS20268	U43752 H.sapiens m
25	306	56.7	522	10	HS20268	U43752 H.sapiens m
26	305.6	56.6	516	10	HS20162	U43752 H.sapiens m
27	305.6	56.6	516	10	HS20162	U43752 H.sapiens m
28	305.6	56.6	516	10	HS20162	U43752 H.sapiens m
29	305.6	56.6	516	10	HS20162	U43752 H.sapiens m
30	305.6	56.6	516	10	HS20162	U43752 H.sapiens m
31	305.6	56.6	527	40	HDWIGHDJA	L23561 Human IGH C
32	304.4	56.4	522	10	HS20269	L23561 Human IGH C
33	304.4	56.4	522	10	HS20269	L23561 Human IGH C
34	304.4	56.4	522	10	HS20269	L23561 Human IGH C
35	304.4	56.4	522	10	HS20269	L23561 Human IGH C
36	304	56.3	516	10	HS20161	L23561 Human IGH C
37	304	56.3	516	10	HS20161	L23561 Human IGH C
38	302	55.9	1553	6	E08434	E08434 CDNA encodl
39	301.4	55.8	525	10	HS20362	L24769 H.sapiens m
40	301.4	55.8	525	10	HS20362	L24769 H.sapiens m
41	298.4	55.3	667	6	I65402	I65402 Sequence 1
42	298.4	55.3	803	10	HDWIGHDJA	L22156 Human (clon
43	298.4	55.3	803	10	HDWIGHDJA	L22156 Human (clon
44	298.2	55.2	525	10	HS20361	L24768 H.sapiens m
45	298.2	55.2	525	10	HS20361	L24768 H.sapiens m

ALIGNMENTS

RESULT 1						
LOCUS	AR000007	9209 bp	DNA			04-DEC-1998
DEFINITION	Sequence 3 from patent US 5736137.					
ACCESSION	AR000007					
NID	g3962538					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 9209)					
AUTHORS	Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rastetter,W.H.					
TITLE	Therapeutic application of chimeric and radiolabeled antilpodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma					
JOURNAL	Patent: US 5736137-A 3 07-APR-1998;					
FEATURES	Location/Qualifiers					
source	1..9209					
BASE COUNT	2239 a 2397 c 2390 g 2183 t					
ORIGIN	/organism="unknown"					

QY	121	TCGAAGGGTTCTGGCTACACCTTACACCACTACTGATGCATTTGGGTGAGGCGGGCCCT	180
Db	169	TCGAAGGCTTCTGGCTACACCTTACACCGGCTACTGATACACTGGGTGAACGAGAGGCTT	228
QY	181	GGCCAAAGCTCTAGATGATGTCGAGAGATGATTCCTTCTGAGAGTAATACTAATACTAAT	240
Db	229	GGACAAAGGCTTGTAGTGATGTGAGAGGTTAATTCCTAGTAGACGGTGTCTGTACTACAAAT	288
QY	241	CAAAAATTCAGAGGAGCGCTCACATTGACTGTAGACATTTCCGCTTAGCACAGGCTTACATG	300
Db	289	GGAAGGCTTCAAACAAAGGACACACTGACTGTAGAACAAATTCCTCCACACAGGCTTCAAG	348
QY	301	GAGCTCAGAGGCTAGATCTAGAGACACATGCGGGTCTACTATTGTGTCAAGAGGGGGTTAC	360
Db	349	CACACTCAGAGGCTTACATCTAGAGACTTGGGGTCTATTACTGTGTCAAGAGAGAGGGCC	408
QY	361	GACGATGGGACTATGCTATTGACTACTAGTGGGGTCAAGGACACCTGGTCAACCGTCTCTCA	420
Db	409	TATGTTTACGACGATGCTATGACTACTGGGGTCAAGGAACCTCAACCGTCTCTCT	468
QY	421	GGCTCCACCAAGGGGCCAATGGGTCTTCCCGCTGGCAACCTCTCCCAAGACACCTTGGG	480
Db	469	GGCAAAAGCACACCCCACTGTCTATTCACATGGGGCCCTGGATCTGCTGCCCAAACTAAC	528
QY	481	GGCACAGCGGGCCCTGGGGTGGCTGTGTCAGACAGACTACTTCCCGCAACGGGTAGCGTGC	539
Db	529	TCCATGTGTAGACCTTGGAAGTGGCTGTGTCAAGGAGGCTATTTCCTGTAGACGATGACAGT	587
RESULT	4		
LOCUS	164458	1572 bp	DNA
DEFINITION	Sequence 23 from patent US 5665357.	PAT	26-SEP-1997
ACCESSION	164458		
NID	92481352		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1572)		
AUTHORS	Rose, M., Samuel, Boot, C., Copley, C., Graham, Paterson, D., Stephen, Hall, S., Margaret, Wright, A., Firman and Blakey, D., Charles.		
TITLE	Antibodies recognizing tumor associated antigen CA 55.1		
JOURNAL	Patent: US 5665357-A 23 09-SEP-1997;		
FEATURES	location/Qualifiers		
source	1..1572		
BASE COUNT	401 a 465 c 378 g 328 t		
ORIGIN			
Query Match	51.0%;	Score 329.4;	DB 6;
Best Local Similarity	75.7%;	Pred. No. 1.2e-80;	Length 1572;
Matches 408;	Conservative 0;	Mismatches 131;	Indels 0;
Gaps	0;		
QY	1	ATGAATGACACTGGGTCATTCCTCTCTGTATCAACAGCTACAGCTGCCACTCCAG	60
Db	49	ATGGATGAGACTATATATATCTCTTTTGTGAGCAACAGTACATATCTCCACTCCAG	108
QY	61	GTCCACTAGTGCAGTCTGGGGCTGAGGTTAAGAAAGCCCTGGGGCTTCACTGAGAGTGTCC	120
Db	109	GTCCAACTGCACACACCTGGGGCTGAACTGTGAACCTGGGGCTTCACTGAGAGTGTCC	168
QY	121	TGCAAGGGTTCTGGCTACACCTTACACCACTACTGATGATTTGGGTGAGGAGGCGCT	180
Db	169	TGCAAGGCTTCTGGCTACACCTTACACCGGCTACTGATACACTGGGTGAAGCAGAGGCT	228
QY	181	GGCCAAAGCTCTAGATGATGTCGAGAGATGATTCCTTCTGAGAGTAATACTAATACTAAT	240
Db	229	GGACAAAGGCTTGTAGTGATGTGAGAGGTTAATTCCTAGTAGACGGTGTCTGTACTACAAAT	288
QY	241	CAAAAATTCAGAGGAGCGCTCACATTGACTGTAGACATTTCCGCTTAGCACAGGCTTACATG	300
Db	289	GGAAGGCTTCAAACAAAGGACACACTGACTGTAGAACAAATTCCTCCACACAGGCTTCAAG	348
QY	301	GAGCTCAGAGGCTAGATCTAGAGACACATGCGGGTCTACTATTGTGTCAAGAGGGGGTTAC	360
Db	349	CACACTCAGAGGCTTACATCTAGAGACTTGGGGTCTATTACTGTGTCAAGAGAGAGGGCC	408
QY	361	GACGATGGGACTATGCTATTGACTACTAGTGGGGTCAAGGACACCTGGTCAACCGTCTCTCA	420
Db	409	TATGTTTACGACGATGCTATGACTACTGGGGTCAAGGAACCTCAACCGTCTCTCT	468
QY	421	GGCTCCACCAAGGGGCCAATGGGTCTTCCCGCTGGCAACCTCTCCCAAGACACCTTGGG	480
Db	469	GGCAAAAGCACACCCCACTGTCTATTCACATGGGGCCCTGGATCTGCTGCCCAAACTAAC	528
QY	481	GGCACAGCGGGCCCTGGGGTGGCTGTGTCAGACAGACTACTTCCCGCAACGGGTAGCGTGC	539
Db	529	TCCATGTGTAGACCTTGGAAGTGGCTGTGTCAAGGAGGCTATTTCCTGTAGACGATGACAGT	587

Dd	289	GAGAACTTCAAGAACAAAGGCCACACTGACTGTATGACAATAAATCCTCCACACACACTTAACG	348
Oy	301	GAGCTCACAGCCTTGAGATCTTGAGGACACTGCCTGTCTACTATTGTGGCAAGAGGGGGTTAC	360
Dd	349	CACACTCACAGCCTTACATCTGAGGACACTCTGGGTCCTATTACTGTGCAAGAGAAGGGCC	408
Oy	361	GACGATATGGGACTATGCTATTGACTACTGACGCGGTCAAAGGACACCCTGTGACCGTCCTCA	420
Dd	409	TATGTTATGACGAATGCTATGACTACTGAGCTGAGGGGTCAAAGAACTCATGCTACCGTCCTCT	468
Oy	421	GCTTCACCAAGAGGCCATCGGTCTTCCCCTGGGACACCTCTCTCAAGACACTCTGGG	480
Dd	469	GCCAAAAGACACCCCCCATCTGTCTATTCACACTGCGCCCTGGATCTGCTGCCAAACTAC	528
Oy	481	GGCACAGCGCCCTGGGCTGCTGCTGTCAAGACTACTTCCCGAACCCTGACGGTGC	539
Dd	529	TCCATGCTGACCTCTGGATGCTGCTGTCAAGGGGCTATTTCCTGAGCACGATGACAGTAGAC	587
RESULT	5		
LOCUS	169485	169485	762 bp DNA PAT 23-DEC-1997
DEFINITION		Sequence 57 from patent US 5677426.	
ACCESSION	169485		
NID	g2831607		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 762)		
TITLE	Fong, S., Hebert, C. Alice, Kim, K. Jin and Leong, S. R.		
JOURNAL	Anti-IL-8 antibody fragments		
FEATURES	Patent: US 5677426-A 5714-Oct-1997;		
	Location/Qualifiers		
	source	1..762	
		/organism="unknown"	
BASE COUNT	183 a	224 c	186 g 169 t
ORIGIN			
Query Match	Best Local Similarity	60.7%; Score 327.8; DB 6; Length 762;	
Matches	408; Conservative	78.0%; Pred. No. 3.3e-80;	
		0; Mismatches 112; Indels 3; Gaps	
Oy	21	TCTCTTTGGTATCAACAGCTACAAAGTGTCCACTCCACAGTCCAACTAAGTCACTGCG	80
Dd	33	TATGTTGCTTTTTTCTATTGTCTAAACGCGCTGACCTGATTCAGCTGCACAGCTGCG	92
Oy	81	GCGTGAAGTAAAGAGCCTGGGGCTTCAGTGAAGGTGTCCTCAAGGGTTCTGGGCTACAC	140
Dd	93	ACCTGAGCTGATGAAGCCTCGGGGCTTCAGTGAAGATATCTGCAAGGCTTCTGGTTATTC	152
Oy	141	CTTCCACGACTACTGATGATTCATTTGGGTAGGCGAGCGCGCTGGCCAAGCTCTAGAGTGAT	200
Dd	153	ATTCTAGTAGCCACTACATGCACTGGGTGAAGCAGGCCATGGAAGAGGCTTGAATGAT	212
Oy	201	CGGAGAGTTGATCTCTTGTGAGAGTAAATCTACTACAAATCAAAAAATCAAGGACCGCT	260
Dd	213	TGGCTACCTTGTATCTTCCATATGGGAAACTACTTCAACCAAGGAAATTCMAAGGCAAGCG	272
Oy	261	CACATTGACTGAGACATTTCCGCTAGGACACAGCTACATGGAAGTGGAGAGCGCTGATGATC	320
Dd	273	CACATTGACTGAGACATCTTCCAGACAGACCAAGCTGCACTCTCAGCAGCCTGACATC	332
Oy	321	TGAGGACACTGCGGCTCTACTATTGTGCAAGAGGGGGTTA--CGACGATGGAGCTATGCG	377
Dd	333	TGATGACTCTGAGCTATCTTCTGTGCAAGAGGGGAGCTATAGATACAAAGCGGACTGCTT	392
Oy	378	TATGACTACTAGTGGGGTCAAGGACCCCTGCTGACCGTCTCTCAGCTCCACCAAGGGCC	437
Dd	393	TTTCGATCTCTGGGGCGGAGGACCAAGGATCAAGCTCTCTCTCCGCTCCACCAAGGGCC	452

Y	438	ATCGGCTCTCCCTTGGACACCTCTCCACAGACACTCTGGGGGCGACAGCGGCGCTGGG	497
Db	438	ATCGGCTCTCCCTTGGACACCTCTCCACAGACACTCTGGGGGCGACAGCGGCGCTGGG	512
Qy	498	CTGCCTGTCAAGSACTACTTCCCCGACACGGTGTAGCGTCTCG	540
Db	513	CTGCCTGTCAAGSACTACTTCCCCGACACGGTGTAGCGTCTCG	555
RESULT	6		
LOCUS	173104	762 bp	DNA
DEFINITION	Sequence 57 from patent US 5686070.		
ACCESSION	I73104		PAT
NID	93009243		23-DEC-1997
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 762)		
TITLE	Doerschuk,C.M., Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R.		
JOURNAL	Methods for treating bacterial pneumonia		
FEATURES	Patent: US 5686070-A 57 11-NOV-1997;		
SOURCE	Location/Qualifiers		
	1..762		
	/organism="unknown"		
BASE COUNT	183 a 224 c 186 g 169 t		
ORIGIN			

Query Match	60.7%;	Score 327.8;	DB 6;	Length 762;
Best Local Similarity	78.0%;	Pred. No. 3.3e-80;		
Matches 408; Conservative	0;	Mismatches 112;	Indels 3;	Gaps 1

Oy	21	TCTCTTTTGGATCAACAGCTACCAAGTGTCCACTCCCAAGCTCCAACTAGACAGTGTGG	80
Db	33	TATGTCTCTTTTCTTATTTGCTACCAACGCTAGCCTAGATTCTAGCTGCACAGCTGTGG	92
Oy	81	GGCTGAGGTTAAGAACCTGGGGGCTTCAGTAAAGGTGTCTGCAGAGGGTCTGTGCCTAAC	140
Db	93	ACCTGACGCTGATGAAGCCCTGGGGGCTTCAGTAAAGATTCTTCGCAAGGCTTCTGGTTATTC	152
Oy	141	CTTCCACAGACACTAGATGACATTTGGGTGAGGAGGGCGGCTGGCCAAAGCTCTAGAGTGAT	200
Db	153	ATTCTAGTGGCCACTTCAATGCACTGGGTGTAAGCAGAGCCATGGAAAGAGCCTTGTAGTGGAT	211
Oy	201	CGAGAGATTGATCTCTTGTGAGAGTAAATACTACTACATCAAAAATTCAAGGAGACGGT	260
Db	213	TGGCTACATTGATCTCTTCCATTGGGAACACTTACCAACGAAATTCAGGGGCAAGGC	272
Oy	261	CACATTGACTGATGACATTTCCGTGAGACAGCCACTATGAGGTCAGACGACCTGAGATC	320
Db	273	CACATTGACTGATGACATCTTCCAGACAGCCACAGCTGCATCTCAGACACTTGACATC	333
Oy	321	TGAGGACACTGGGGTCTACTATTGTGCAAGAGGGGGTTA--CGACGGATGGACTATGC	377
Db	333	TGATGACTCTGGAGTCTTCTGTGCAAGAGGGGACTATGATTAACAAGCGCACTGGTT	392
Oy	378	TATTGACTAGTGGGGTCAAGGCAACCCGTGACCGTCTCCACAGCTCCACACAGGGGCC	437
Db	393	TTTGCATCTCTGGGGGCGCAGGGACACAGCTACCGCTCTCTCCGCTTCCACCAAGGGGCC	455
Oy	438	ATCGGTTCTTCCCTCGGACACCTCTCTCCAAAGACACTCTGGGGGACAGAGGACCTTGGG	497
Db	453	ATCGGTTCTTCCCTCGGACACCTCTCTCCAAAGACACTCTGGGGGACAGAGGACCTTGGG	512
Oy	498	CTGCTGCTCAAGACACTTCTCCCGAAGCCGGTGAAGCTGTGC	540
Db	513	CTGCTGCTCAAGACACTTCTCCCGAAGCCGGTGAAGCTGTGC	555

LOCUS	179289	762 bp	DNA	PAT	20-MAR-1998
DEFINITION	Sequence 57 from patent US 5707622.				
ACCESSION	179289				
NID	93207579				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 762)				
TITLE	Fong,S., Hebert,C,Alice, Kim,K.Jin and Leong,S.R.				
JOURNAL	Methods for treating ulcerative colitis				
FEATURES	Patent: US 5707622-A 57 13-JAN-1998;				
SOURCE	Location/Qualifiers				
	1..762				
	/organism="unknown"				
BASE COUNT	183 a	224 c	186 g	169 t	
ORIGIN					

Query Match	60.7%;	Score 327.8;	DB 6;	Length 762;
Best Local Similarity	78.0%;	Pred. No. 3.3e-80;		
Matches 408; Conservative	0;	Mismatches 112;	Indels 3;	Gaps 1

Oy	21	TCCTCTTTGGTATCAACAGCTACACAGTGCATCCATCCAGGCTCCAACTAGTCAAGTGG	80
Db	33	TATCTTCGTTTTTCTATTGCTACAAACCGGTCAGCTGATATAGCTGCACGACGTGG	92
Oy	81	GCGTAGAGTTAAGAACCCCTGGGGCTTCACTGTAAGAGTGTCTCGCAAGGGTTCTGGCTACAC	14
Db	93	ACCTGACCTCATGATACCCCTGGGGCTTCACTGTAAGATATCTCGCAAGGCTTCTGGTTATTC	15
Oy	141	CTTACACGAGTATGGATGATCTGGGTGGAGAGGCGCTGGGCCAAGCTGTACAGTGGAT	20
Db	153	ATTATGATGACCACTAATATGACTCGGTGACACAGCCATGGAAGACCTTATAGTGGAT	21
Oy	201	CGAGAGATTGATCCTTCTGAGAGTAACTACTACTACATCAATAAATAATCAAGGAGCGT	26
Db	213	TGGCTAATTGATCTCTCCAAATGGTGAACACTACTACACAGAAATTCAGGGCAAGCG	27
Oy	261	CACATTCAGCTGTAGATATTTCCGGTAGACACAGCCCTAATGAGGTGACGAGCTGTAGATC	32
Db	273	CACATTCAGCTGTAGACACTCTCCAAATGGTGAACACTACTACACAGAAATTCAGGGCAAGCG	33
Oy	321	TGAGGACACTGCGGCTACTATTGTGCAAGAGGGGTGATG---CGACGAGTGGACTATGC	37
Db	333	TGATGACTCTGCACTGATTTCTGTGCAAGAGGGGACTATGATATCAACGGCCACTGTT	39
Oy	378	TATGTACTACTGGGGTCAGAGGCAACCTGTACCGTCTCCACCTCCACCAAGGGCCC	43
Db	393	TTTGTGATGTGGGGGCGCAGGAGCAACGCTACCGTCTCTCGCTCCACCAAGGGCCC	45
Oy	438	ATCGGCTTTTCCCTGGGCAACCTCTCTCAAGACACCTGTGGGGGCGACAGCGGCTCTGGG	49
Db	453	ATCGGCTTTTCCCTGGGCAACCTCTCTCAAGACACCTGTGGGGGCGACAGCGGCTCTGGG	51
Oy	498	CTGCTGGGTCAAGGACTACTTTCCTCCGAACCGGTACAGGTCTCG	540
Db	513	CTGCTGGGTCAAGGACTACTTTCCTCCGAACCGGTACAGGTCTCG	555

RESULT	8			
LOCUS	187063			
DEFINITION	187063	762 bp	DNA	
ACCESSION	187063	Sequence 57 from patent US 5702946.	PAT	20-MAR-1998
NID	g3206781			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 762)			
AUTHORS	Doerschuk,C.M., Fong,S., Hebert,C.Alice, Kim,K.Jin and Leong,S.R			
TITLE	Anti-IL-8 monoclonal antibodies for treatment of inflammatory			

disorders
 JOURNAL Patent: US 5702946-A 57 30-DEC-1997;
 FEATURES Location/Qualifiers
 source 1..762
 BASE COUNT 183 a 224 c 186 g 169 t
 ORIGIN

Query Match 60.7%; Score 327.8; DB 6; Length 762;
 Best Local Similarity 78.0%; Pred. No. 3.3e-80;
 Matches 408; Conservative 0; Mismatches 112; Indels 3; Gaps 1;

21 TCTCTCTGTATCAACAGCTACAGAGTGTCCAGCTCCAGCTACAGTGTCTGG 80
 33 TATGTCGTTTTCATGTACAAAGCGTACGCTAGATTCAGCTGACAGCTGG 92
 81 GGCTGAGTTAAGAACCTGGGGCTTCAGTGAAGTGTCTCCAGAGGTTCTGGCTAC 140
 93 ACCTGAGCTGATGAAGCTGGGGCTTCAGTGAAGATATCTCCAGAGCTTGTGTTATTC 152
 141 CTTCACCACTACTGATGATGCTGGTGAAGGAGCGGCTGGCCAGCTAGAGTGAT 200
 153 ATTCAGTACCACTACATGCTGCTGGAAGAGAGCCATGGAAAGCTTGAGTGAT 212
 201 CGAGAGATTGATCTTCTGAGAGTATATCTACTACATCAAAATTCAGAGGAGCGT 260
 213 TGGTACATGATATCTTCCATGTAAGTGAATCTACTTCAACAGAAATTCAGAGGCAAGC 272
 261 CACATTGACTGATGACATTCGCTGATGACAGAGCTGATGAGCTGAGAGCTGATGATC 320
 273 CACATTGACTGATGACATTCGCTGATGACAGAGCTGATGAGCTGATGATC 332
 321 TGAGGACACTGGGCTACTATTTGTCAGAGGGGGTAA---CGAGGATGGAGTATGC 377
 333 TATGACTCTGCAAGTCTATTTCTGTCAGAGGGGACTATGATTAACGGGAGCTGTT 392
 378 TATTGACTACTGGGGTCAAGGACACCTGCTGACCTCTCTGAGCTCCACCAAGGGCCC 437
 393 TTTGATGCTCTGGGGGCGAGGAGCACAGCTCAACGCTCTCTCGCTCCACCAAGGGCCC 452
 438 ATGCGTCTTCCCTGGGACCTCTCTCAAGAGACCTCTGGGGGCGACAGCGCCCTGGG 497
 453 ATGCGTCTTCCCTGGGACCTCTCTCAAGAGACCTCTGGGGGCGACAGCGCCCTGGG 512
 498 CTGCGTGGTCAAGGACTACTTCCCGAAGCGGAGCGGTGCG 540
 513 CTGCGTGGTCAAGGACTACTTCCCGAAGCGGAGCGGTGCG 555

RESULT 9
 HUMIGHDUC 531 bp mRNA PRI 09-NOV-1994
 LOCUS Human Igh chain VDJC region mRNA, partial cds.
 DEFINITION L23555
 ACCESSION 949585
 NID 949585
 KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain.
 SOURCE Homo sapiens (individual isolate Donor B) adult peripheral blood
 CDNA to mRNA.

ORGANISM Homo sapiens
 Eukaryote; mitochondria; eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS Chai, S.K., Kasalan, M.T., Ikematsu, H., Kim, M.Y. and Casali, P.
 TITLE VH-D-JH gene sequences of mab produced by human B-1a, B-1b, and B-2
 cells
 JOURNAL Unpublished (1994)
 FEATURES Location/Qualifiers
 source 1..531
 /organism="Homo sapiens"
 /isolate="Donor B"
 /db_xref="taxon:9606"
 /cell_line="417.32F4.8.5"

/cell_type="B-cell, EBV-transformed and fused with
 human-mouse heterohybridoma F3b6"
 /dev_stage="adult"
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 /note="G00-118-731"
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 /gene="IGH"
 /note="xxx"
 /codon_start=3
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 /db_xref="GDB:G00-118-731"
 /product="Immunoglobulin heavy chain"
 /db_xref="PID:955395"
 /translation="EFMDWTIRILFLENAATGTHAEVOLVOSGAEVKKPGTTRISK
 VSGYTFDYHMYROAAGKLEWGLVDPEGDGATVPEKFGRIITADISTDAVM
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 SGTATAGCLYKDNLS"

V_segment 66..359
 /gene="IGH"
 /note="G00-118-731"
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 /note="xxx; G00-118-731"
 /product="Immunoglobulin heavy chain"
 360..383
 /gene="IGH"
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 384..428
 /gene="IGH"
 /note="G00-118-731"
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 /gene="IGH"
 /note="G00-118-731"
 BASE COUNT 123 a 152 c 153 g 103 t
 ORIGIN

Query Match 60.4%; Score 326.2; DB 10; Length 531;
 Best Local Similarity 77.1%; Pred. No. 8.9e-80;
 Matches 397; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

1 ATGAATGACCTGGGCTATCTCTTGTATCAACAGCTACAGTGTCCACTCCAG 60
 9 ATGACTGACCTGGAGATCTCTTGTGAGGACAGCTACAGGACCCAGCCGAG 68
 61 GTCCAACTAGTCACTTGGGGCTAGGTTAAGAGCTGGGGCTTCAAGTGAAGTTC 120
 69 GTCCAACTAGTCACTTGGGGCTAGGTTAAGAGCTGGGGCTTCAAGTGAAGTTC 128
 121 TCCAAAGGTTTGGCTACACTTCCACAGCTCTGATGATGGGTGAGGAGCGGCT 180
 129 TCCAAAGGTTTGGCTACACTTCCACAGCTCTGATGATGGGTGAGGAGCGGCT 188
 181 GGCACAGCTTGTAGTGTGAGAGATGATGATCTTGTGAGAGTAAATCTACTACAT 240
 189 GGAAGAGGCTTGAATGGGTGAGTGTGATCTGAAAGATGTAAGCATCTACCCA 248
 241 CAAAATTCAGAGGAGCGGTCACTGATGATGATGATGATGATGATGATGATGATG 300
 249 GGAAGTTCAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 308
 301 GAGCTCAGAGCTGAGATCTGAGGAGCACTGGGCTCTACTATTTGCAAGAGGGTTAC 360
 309 GAGGTGAGAGCTGATCTGAGGAGCACTGGGCTCTACTATTTGCAAGAGGGTTAC 368
 361 GAGGATGAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 369 ATATATCCCCACCGGATGAGCTGTGGGCGCAAGGAGGACACGCTACCGTCTCTCA 428

QY 421 GCCTGCACAGGGCCATGCTTCCCTGCGACCTCTCCAGACGACCTCTGGG 480
 DB 429 GCCTGCACAGGGCCATGCTTCCCTGCGACCTCTCCAGACGACCTCTGGG 488
 QY 481 GGCACAGCGGCGCTGGCTGCTGCTCAGAGACTA 515
 DB 489 GGCACAGCGGCGCTGGCTGCTGCTCAGAGACTA 523
 RESULT 10
 HUMIGHDUA 531 bp mRNA PRI 09-NOV-1994
 LOCUS Human IGH chain VDJC region mRNA, partial cds.
 DEFINITION L23555
 ACCESSION 9499585
 NID C-region; D-region; J-region; V-region; Immunoglobulin heavy chain.
 KEYWORDS Homo sapiens (individual isolate Donor B) adult peripheral blood
 SOURCE CDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryote; mitochondria eukaryotes; Metazoa; Chordata;
 Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 531)
 AUTHORS Chal,S.K., Kasalan,M.T., Ikematsu,H., Kim,M.Y. and Casali,P.
 TITLE VH-D-JH gene sequences of mab produced by human B-1a, B-1b, and B-2
 cells
 JOURNAL Unpublished (1994)
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /isolate="Donor B"
 /db_xref="taxon:9606"
 /cell_line="417.32P4.8.5"
 /cell_type="B-cell; EBV-transformed and fused with
 human-mouse heterohybridoma F3B6"
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 Best Local Similarity 77.1%; Pred. No. 8.9e-80;
 Matches 397; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
 QY 1 ATGAATGACCTGGGTCTCTCTTCTGATCAACAGCTACAGTGTCCACTCCAG 60
 DB 9 ATGAGCTGACCTGGAGATCTCTTCTGAGGAGCAGCTACAGGACCCAGCCGAG 68
 QY 61 GTCCACTAGTGCAGCTGCTGGGCTGAGTTAGAACCTGGGGCTTCATGAAGTGTCC 120
 DB 69 GTCCAACTGTATAGTCTGGGCTGAGTGAAGAACCTGGGACTACATGAATACTCC 128
 QY 121 TGCAGGTTCTGCTACACCTTACACCACTGATGATGATGGGTGAGAGGCGCT 180
 DB 129 TGCAGGTTCTGATACACCTTACACCACTGATGATGATGGGTGAGAGGCGCT 188
 QY 181 GGCACAGCTCTAGAGTGGATCGAGAGATTGCTCTGAGAGTAATCTAATCAAT 240
 DB 189 GGAAGAGGCTTGAAGTGGGAGTGTGATCTGAGAGTGAAGTGAAGCAATCTACCA 248
 QY 241 CAAATTCAGAGGAGCGCTACATTCATGATGATGATGATGATGATGATGATGAT 300
 DB 249 GAGCAATTCAGAGGAGCGCTACATTCATGATGATGATGATGATGATGATGATGAT 308
 QY 301 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 309 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 368
 QY 361 GAGGATGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 369 AATATATCCCGCCACCGGTATGAGCTGCTGGGCAAGGAGACAGGCTACCGTCTCTCA 428
 QY 421 GCCTGCACAGGGCCATGCTTCCCTGCGACCTCTCCAGACGACCTCTGGG 480
 DB 429 GCCTGCACAGGGCCATGCTTCCCTGCGACCTCTCCAGACGACCTCTGGG 488
 QY 481 GGCACAGCGGCGCTGGCTGCTGCTCAGAGACTA 515
 DB 489 GGCACAGCGGCGCTGGCTGCTGCTCAGAGACTA 523
 RESULT 11
 MUSIGH1H1 1544 bp mRNA ROD 25-APR-1996
 LOCUS Mouse mRNA for immunoglobulin gamma-3 V-D-J region and secreted
 DEFINITION constant region, complete cds.
 ACCESSION D14625
 NID 9286089
 KEYWORDS Immunoglobulin gamma-3 secreted C-region; Immunoglobulin V region;
 Immunoglobulin gamma-3 heavy chain; Immunoglobulin gamma-3 heavy
 chain precursor.
 SOURCE Mus musculus (strain: MRL/MPJ-1pr/1pr, library: pBluescript KS(+))
 adult CDNA to mRNA, clone pB1H1.
 ORGANISM Mus musculus
 Eukaryote; mitochondria eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Rodentia; Scurionath; Muridae;
 Murinae; Mus.
 REFERENCE 1 (bases 1 to 1544)
 AUTHORS Takahashi,S., Itoh,J., Nose,M., Ono,M., Yamamoto,T. and Kyogoku,M.
 TITLE Cloning and cDNA sequence analysis of nephritogenic monoclonal
 antibodies derived from an MRL/lpr lupus mouse
 JOURNAL Mol. Immunol. 30 (2), 177-182 (1993)
 MEDLINE 93156722
 REFERENCE 2 (sites)
 AUTHORS Ono,M., Yamamoto,T., Kyogoku,M. and Nose,M.
 TITLE Sequence analysis of the germ-line VH gene corresponding to a
 nephritogenic antibody in MRL/lpr lupus mice
 JOURNAL Clin. Exp. Immunol. 100 (2), 284-290 (1995)
 MEDLINE 95262286
 REFERENCE 3 (bases 1 to 1544)
 AUTHORS Nose,M.

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OY      523  GAACCGGTGACGGTGTGC 540
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RESULT 13
LOCUS   HOMIGHPEAH
DEFINITION
Human (Hybridoma H210) anti-hepatitis A IgG variable region,
constant region, complementarity-determining regions mRNA, complete
cds.
ACCESSION M87789
NID        g185361
KEYWORDS   complementarity-determining region; constant region; immunoglobulin
           gamma-chain; immunoglobulin heavy chain; variable region.
           Homo sapiens cDNA to mRNA.
ORGANISM   Homo sapiens
            Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrate; Euteria; Primates; Catarrhini; Hominiidae; Homo.
            1 (bases 1 to 1599)
REFERENCE  Lewis,A.P., Lemon,S.M., Barber,K.A., Murphy,P., Parry,N.R.,
            Peakman,T.C., Sims,M.J., Worden,J., and Crowe,J.S.
            Rescue, expression, and analysis of a neutralizing human
            anti-hepatitis A virus monoclonal antibody
            J. Immunol. 151 (5), 2829-2838 (1993)
JOURNAL   93367243
MEDLINE
FEATURES
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gene

misc_feature

misc_feature

mat_peptide

3'UTR

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Best Local Similarity 75.4%; Pred. No. 1.7e-78;
Matches 421; Conservative 0; Mismatches 119; Indels 18; Gaps 1;

QY 1 ATGAATGACACCTGGGCTATCTCTTCTGTATCAACAGTACAAAGTGTCCACG 60
DB 35 ATGAGACTGGACCTGGAGGCTCTCTTGTGTGGACAGTAAAGGTCCACG 94
QY 61 GTCCAACTAGTACAGTGTGGGCTGAGGTTAAGAGCTGGGGCTGTAAGAGTGTCC 120
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QY 121 TGCAGAGGTTCTGGCTACACCTTCACCAAGTACTGATGATGAGTGGAGGAGGCT 180
DB 155 TGCAGAGCTATGAGGACCTTCAGCAACTATGCTATGAGTGGGAGGAGGCT 214
QY 181 GCGCAAGCTTAGAGTGTGAGAGATGATGCTTCTGTAGAGTAACTACTAAT 240
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DB 335 GAGCTGATCAGCCTGAGATCTGAGAGACAGGCGGTATTTACTGTGGAGAGAGCTGATC 394
QY 357 -----TTACGAGAGTGGAGTATGCTATTTGACTCTGAGGCTCAAGCACC 402
DB 395 AGGACAGCAATTTTGAACGGGCGGCTGTGCTGAGTCCCTGTGGGAGGAGGAGC 454
QY 403 CTGCTACCGCTCTCTAGAGCTCCACCAAGGGCCCATGGGCTCCCGCTGGAGCCTTC 462
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QY 523 GAACCGGTGACGGTGTGCG 540
DB 575 GAACCGGTGACGGTGTGCG 592

RESULT 14

LOCUS 158595 3282 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 154 from patent US 5652138.
ACCESSION 158595
NID 92477833

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 3282)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
JOURNAL Patent: US 5652138-A 154 29-JUL-1997;
FEATURES
source 1.3282 Location/Qualifiers
BASE COUNT 710 a 1109 c 864 g 599 t
ORIGIN

Query Match 59.0%; Score 318.4; DB 6; Length 3282;
Best Local Similarity 75.1%; Pred. No. 1.3e-77;
Matches 419; Conservative 0; Mismatches 121; Indels 18; Gaps 1;

QY 1 ATGAATGACACCTGGGCTATCTCTTCTGTATCAACAGTACAAAGTGTCCACG 60
DB 15 ATGAGACTGGACCTGGAGGCTCTCTTGTGTGGACAGTAAAGGTCCACG 74
QY 61 GTCCAACTAGTACAGTGTGGGCTGAGGTTAAGAGCTGGGGCTGTAAGAGTGTCC 120
DB 75 GTTACAGTGTGCTAGTGTGGGCTGAGGTTAAGAGAGCTGGGCTGTAGAGTGTCT 134
QY 121 TGCAGAGGTTCTGGCTACACCTTCACCAAGTACTGATGATGAGTGGAGGAGGCT 180
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QY 463 TCCAAAGACACCTCTGGGGGACAGCGGCTGGGCTGCTGTCAAGAGTACTTCCC 522
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DB 555 GAACCGGTGACGGTGTGCG 572

RESULT 15

LOCUS 158596 13254 bp DNA PAT 14-AUG-1997
DEFINITION Sequence 156 from patent US 5652138.
ACCESSION 158596
NID 92477834

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 13254)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
JOURNAL Patent: US 5652138-A 156 29-JUL-1997;
FEATURES
source 1.13254 Location/Qualifiers
BASE COUNT 3206 a 3559 c 3251 g 3238 t
ORIGIN

Query Match 59.0%; Score 318.4; DB 6; Length 13254;
Best Local Similarity 75.1%; Pred. No. 1.4e-77;
Matches 419; Conservative 0; Mismatches 121; Indels 18; Gaps 1;
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QY 121 TGCAGGGTTCGCTACACCTTCACAGCTACTGATGCATTGGGTGAGGAGGGCCT 180
Db 2570 TGTCAAGCTTCTGATACAGATTCAGTAACCTTGTATTCAATGGGTGGCCAGCCCC 2629
QY 181 GGCCAACTAGAGTGAAGAGAGATTGATCCTCTGAGAGTAATACTACTACAAT 240
Db 2630 GGACAGAGTTGATGATGATGATGATCAATCCTTACAGGAACAAAGAAATTTCA 2689
QY 241 CAAAATTCAGAGGAGGAGGAGTGCATATTCAGTACATTCGCTAGCACAGCCTACATG 300
Db 2690 GCGAAGTTCAGAGAGAGATCACTTTCACGGGACACATCCGCAACACAGCCTACATG 2749
QY 301 GAGCTCAGCAGCCTGAGATCTGAGAGACACTGGGTCTACTATTGTGCAAGAGGGGTAC 360
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QY 361 GACGAGTGGACTATGC-----TATTGACTACTGGGGTCAAGCAAC 402
Db 2810 TATAGTTGGATGATTCCTCCAGGACATTAATATGAGAGCTGGGGGCAAGGAAC 2869
QY 403 CTGGTACACCTCTCTCAGCCTCCACCAAGGGCCATCGGTCTCCCTGGCACCTGC 462
Db 2870 ACGGTATCTGAGCTCAGCTTCCACCAAGGGCCATCGGTCTCCCTGGCACCTGC 2929
QY 463 TCCAAGAGCACCCTTGGGGGACACAGCGGCCCTGGGCTGCTGTGCAAGAGACTACTCCGC 522
Db 2930 TCCAAGAGCACCCTTGGGGGACACAGCGGCCCTGGGCTGCTGTGCAAGAGACTACTCCGC 2989
QY 523 GAACCGGTGACGGTTCG 540
Db 2990 GAACCGGTGACGGTTCG 3007
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Search completed: May 11, 1999, 12:00:33
Job time: 1480 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:14 ; Search time 479.58 Seconds

(without alignments)
1/17.605 Million cell updates/sec

Title: US-08-700-737-18

Perfect score: 540
Sequence: 1 ATGAAATGCACCTGGTGCAT.....CCGACCGGTGACGCTGTCG 540

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database :

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2: em_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	209.2	38.7	387	22	AA569186	nm30d10.s
2	201.4	37.3	310	30	AI180569	uc70f09.r

C	3	198	36.7	461	31	AI201426	AI201426
	4	184.6	34.2	432	28	AI268604	AI268604
	5	180.4	33.4	424	31	AI007196	AI007196
	6	170.2	31.5	256	17	AA300605	AA300605
	7	157.8	29.2	437	13	HS053086	HS053086
	8	157.4	29.1	279	17	AA300571	AA300571
	9	152	28.1	366	19	AA378312	AA378312
	10	152	28.1	366	19	AA378312	AA378312
	11	148.4	27.5	379	21	AA291381	AA291381
	12	148.4	27.5	431	25	AA710970	AA710970
	13	146.4	27.1	287	11	T27609	T27609
	14	144	26.7	223	12	H68593	H68593
	15	143.2	26.5	291	18	AA377074	AA377074
	16	139.6	25.9	233	16	AA170256	AA170256
	17	137.4	25.4	238	11	T29670	T29670
	18	137	25.4	265	18	AA377128	AA377128
	19	136.2	25.2	199	12	H61366	H61366
	20	135.6	25.1	267	18	AA360197	AA360197
	21	131.6	24.4	346	13	HS053085	HS053085
	22	123.2	22.8	266	24	AA402547	AA402547
	23	122.6	22.7	367	10	T60021	T60021
	24	120.6	22.3	230	24	AA428970	AA428970
	25	120	22.2	271	23	AI214557	AI214557
	26	118.2	21.9	209	11	T28938	T28938
	27	115	21.3	372	25	AA581192	AA581192
	28	113.6	21.0	188	19	AA383972	AA383972
	29	112	20.7	230	18	AA346313	AA346313
	30	111.4	20.6	385	11	R86288	R86288
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	33	101	18.7	271	18	AA369101	AA369101
	34	100.6	18.6	630	27	AA895088	AA895088
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	38	96.6	17.9	238	21	AA505044	AA505044
	39	95.4	17.7	474	31	AI147237	AI147237
	40	91	16.9	485	29	AA988730	AA988730
	41	89.2	16.5	430	11	R72787	R72787
	42	85.8	15.9	432	21	AA544384	AA544384
	43	84	15.6	304	17	AA300945	AA300945
	44	82.8	15.3	397	20	AA472093	AA472093
	45	79.8	14.8	488	29	AA948436	AA948436

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION nm30d10.s1 NCI-CGAP_L1P2 Homo sapiens CDNA clone IMAGE:1061663
Similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-1 REGION (HUMAN);.
mRNA sequence.
ACCESSION AA569186
NID 92342240
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

to gb:M18512 IG HEAVY

DEFINITION NC_1_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943722 3'

95/3000.41 NC1_CONF_F120 HUMO SAPIENS UUNA C106E.1375/22 3
similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION

ACCESSION	(HUMAN); contains Alu repetitive element; mRNA sequence.
NID	A1201426
RETWORDS	G3754032
SOURCE	EST.
ORGANISM	human.
JOURNAL COMMENT	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 461) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
REFERENCE AUTHORS TITLE	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Insert length: 608 Std Error: 0.00 Seq primer: -400P from GIBCO. Location/Qualifiers 1..461
FEATURES SOURCE	/organism="Homo sapiens" /note="Organ: prostate; Vector: PT7r3D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP_Pr72 was prepared, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 98508-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and W. Fatima Bonaldo." /db_xref="taxon:9606" /clone="IMAGE:1943722" /clone_1lb="NCI_CGAP_Pr78" /sex="male" /dev_stage="adult" /lab_host="DH10B"
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Best Local Similarity	76.4%; Pred. No. 8.3e-49;
Matches 243; Conservative	0; Mismatches 75; Indels 0; Gaps 0;
OY	35 CAACGCTACAAGTGTCACACTCCACGGGTCCAACCTATGTCAGCTGGGGCTGAGGTTAAGA 94
DB	461 CACCAGCTCAAGGTGCCACACTCCACGGGTGCAGCTGTGCGGCTAGGTGAAGA 402
OY	95 AGCCTGGGGCTTCACTGAAGGTGTCTCTCAAGGGTTCTGGCTACACTTCCACAGTACT 154
DB	401 AGCCTGGGGCTTCACTGAAGGTGTCTCTCAAGGGTTCTGGCTACACTTCCACAGTACT 342
OY	155 GGATCATTTGGGTGAGCGAGGGCGCTGCCCAAAGCTCTAGAGTGGATGGAGAGATTGATC. 214
DB	341 ATATCACTAGGTGGTGCAGACGGCCCCCTGGACAAGAGCTTGGGTGATGGAGACGGAATCAAC 282
OY	215 CTTCGAGAGTAATCTCAATCAATCAAAAATTCAAGGAGCGCTGCATTTGACTGTAG 274
DB	281 CTAAACAGTGTGGCGCAAACTCTAGTCAGCAAGAAATTTCAAGGGAGAGAGTCCATGTACAGGG 222
OY	275 ACATTTCCGCTGACACAGCCTTACATGAGAGCTCAGACGCTGAGATCTGAGGACACTGGGG 334
DB	221 ACGCTCCATCAGCACACACCTTACAGGAGCTGAGAGCCTGAGATCTGAGGACACGGCCA 162
OY	335 TCTACTANTGTGCAAGAG 352
DB	161 CGTATTACTGTGCGAGAG 144

LOCUS	A1268604	432 bp	mRNA	EST	17-NOV-1998				
DEFINITION	9c47a10.x1 NCI CGAP Llus Homo sapiens cDNA clone IMAGE:1911642 3' similar to gb:X14584 IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN); contains MSRI.c1 MSRI repetitive element ; , mRNA sequence.								
ACCESSION	A1268604								
NID	93887771								
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;								
	Primates; Catarrhini; Hominoidea; Homo.								
REFERENCE	1 (bases 1 to 432)								
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.								
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index								
JOURNAL	Unpublished (1997)								
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: www-bio.llnl.gov/bdrp/image/image.html								
FEATURES	Seq primer: -40UP from GIBCO High quality sequence stop: 409.								
source	Location/Qualifiers								
	1..432								
	/organism="Homo sapiens"								
	/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library is normalized. Library was constructed by Bento Soares and W. Fatima Bonaldo."								
	/db_xref="taxon:9606"								
	/clone="IMAGE:1911642"								
	/clone_lib="NCI CGAP Llus"								
	/tissue_type="carcinoid"								
	/lab_host="DH10B"								
BASE COUNT	92 a	122 c	127 g	91 t					
ORIGIN									
Query Match	34.2%	Score 184.6;	DB 31;	Length 432;					
Best Local Similarity	65.7%;	Pred. No. 7.7e-45;							
Matches 287;	Conservative 0;	Mismatched 144;	Indels 6;	Gaps 1;					
Db	43 ACAAGTCCACTCCCAAGTCCTCAGTGTGGGCTGAAGAGCTGGG 102								
Db	2 AAAGTGTCAGTGTGAGGTGCACCTGTGGAGTTGGGGGAGAACTTGGTCCAGCTGGG 61								
Db	103 GCTTCAGTGAAGGTGTCTGCAGAGGGTTCTGGCTACACCTTCACCAGCTACTGATCAT 162								
Db	62 GGGTCCCTGAGACTCTCTGTCGACACCTCTGGATTCACTTTAGACGATGCCATGAAC 121								
Db	163 TGGGTGAGGACGAGGCGCTGGGCCAACGTTTAGAGTGGATCGGAGAGATTGATCTTCTGAG 222								
Db	122 TGGGTCCCGGACGGCTCCAGGGGAAGGGGCTGAGTGGTCTATTGTTAATTAACGGTGGG 181								
Db	223 AGTAATACTAATAATCAAAAATTCAGAGGAGCGCACATTGACGTGACATTTCC 282								
Db	192 ACTCAAACACACACGACACTCCGTGAAGGGCCGTTTATCATCTCCAGAGACAATTC 241								
Db	283 GCTACACAGGCTACATGAGAGCTGACGACCTGAGATCTGAGACACTGCGGTACTAT 342								

BASE COUNT	85 a	68 c	77 g	64 t
------------	------	------	------	------

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3016699056
Fax: 3016699423
Email: arkerlavet@igmr.org
For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgl/hgl.html>)
Seq primer: M13 Reverse.

FEATURES	location/qualifiers
source	1. . 279

mRNA	<1.	>279		
BASE COUNT	63 a	74 c	85 g	56 t
ORIGIN				1 others

Query Match	29.1%;	Score 157.4;	DB 17;	Length 279;
Best Local Similarity	77.0%;	Pred. No. 8.1e-37;		
Matches 191; Conservative	0;	Mismatches 57;	Indels 0;	Gaps 0;

Qy	1	ATGAAATCACCCTGGGTCATTCTCTCTGTGATACACAGCTACAAATGTCACCTCCAG	60
Db	32	ATGAGCTGACCTGGAGGATCCTTCTCTGTGGCAGACGCAAGGAGCCCACTCCAG	91
Qy	61	GTCCAACTAGTGCAGTCTGGGGCTGAGGTTAAGAAGCTGGGGCTTCAGTGAAGGTGCC	120
Db	92	GTGAGCTGTGTGCAGTCTGGGGCTGAGGTGAAGAAGCTGGGGCTTCAGTGAAGGTGCC	151
Qy	121	TGCAAGGGTTTGCTACACCTTACACGAGTACAGATGATGCTTGGGTGAGGAGGGGCGCT	180
Db	152	TGCAAGGCTTTTGATACACTTACACGGGCTACTATATGCACTGGGTGCGACAGGCCCT	211
Qy	181	GGCCACGCTTAGAGTGGATCGAGAGATTGATCCTTCTGAGACTTAATTAATACTACAT	240
Db	212	GGACAAGGGCTTNGATGGATGGAGTGAATCAACCTTAAAGGTGGCACAAACTATGCA	271
Qy	241	CAAAATT	248
Db	272	CAGAGTT	279

RESULT	9
AA378312	
LOCUS	AA378312
DEFINITION	EST19101 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to Immunoglobulin gamma 1 heavy chain, C region, mRNA sequence.
ACCESSION	AA378312
NID	G2030651
KEYWORDS	EST.
SOURCE	human.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel.: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi.html>)
Seq primer: M13 Reverse,
<http://www.tigr.org/qualitycontrol/>

FEATURES	SOURCE
location/Qualifiers	1.366
/organism="Homo sapiens"	
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"	
/db_xref="ATCC (inhost):182729"	
/db_xref="taxon:9606"	
/clone_lib="Synovial sarcoma"	
/sex="female"	
/tissue_type="synovial membrane"	
/dev_stage="adult, 20 yrs"	
<1.366	
77 a 114 c 101 g 72 t 2 others	
BASE COUNT	
ORIGIN	

Query Match	28.1%	Score 152;	DB 18;	Length 366;
Best Local Similarity	96.3%	Pred. No. 3.5e-35;		
Matches 155; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

QY	380	TTGACTACTGGGGGTCAGAGGACACCTGGTCACCGTCTCTCTACGCTCCACCAAGGGCCAT	439
Db	120	TTGAGTACTGGGGGCAAGGAGACCTGGTCACCGTCTCTACGCTCCACCAAGGGCCAT	179
QY	440	CGGTCCTCCCGCTGGGCAACCCCTCTCCAAAGACACTCTGGGGGGGACAGCGGCCCTGGGCT	499
Db	180	CGGTCCTCCCGCTGGGCAACCCCTCTCCAAAGACACTCTGGGGGGGACAGCGGCCCTGGGCT	239
QY	500	GCTGTGTCAGGACTACTTCCCGCAACCGGAGACGCTGTGCG	540
Db	240	GCTGTGTCAGGACTACTTCCCGCAACCGGAGACGCTGTGCG	280

RESULT	10
AA987559	
LOCUS	
DEFINITION	AA987559 336 bp mRNA EST 23-JUL-1998
	OT83901.s1 NCI_CCAP.Lu5 Homo sapiens cDNA clone IMAGE:1602460
	similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA

ACCESSION	AA987559
NID	g3172923
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 336)
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
Contact:	Robert Strausberg, Ph.D.
Tel.:	(301) 496-1550
Email:	Robert_L_Strausberg@nih.gov

Query Match 27.1%; Score 146.4; DB 11; Length 287; Best Local Similarity 73.2%; Pred. No. 1.5e-33; Matches 186; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 ATGAATGACACCTGGGCTATCTCTTGGTATCAACAGCTACAGTCCACTCCAG 60
 DB 14 ATGAGCTGACCTGGAGATCTCTTGGTGGGACAGCAGCAAGAGCCCTCCAG 73
 QY 61 GTCCACTAGTGGAGTGGGGCTGAGTTAAGAGCTGGGGCTGAGTGAAGGTCTC 120
 DB 74 GTGACCTGTGCTGAGTGGGGCTGAGTGAAGAGCTGGGGCTGAGTGAAGGTCTC 133
 QY 121 TGCAGAGGCTGCTGACCTGACCTCACCAGCTAGTGAAGTGGTGAAGGAGGCTC 180
 DB 134 TGCAGAGCTGCTGAGTGGGGCTGAGTGAAGAGCTGGGGCTGAGTGAAGGTCTC 193
 QY 181 GGCACACGCTAGAGTGGAGTGGAGAGTGGTCTCTGAGAGTAACTACTAAT 240
 DB 194 GGACAGAGGCTGATGATGAGTGGAGTGGAGAGCTGGAGTGGAGTGGAGTGGAG 253
 QY 241 CAAATATTCAGGG 254
 DB 254 CGAAGTTTGGG 267

RESULT 14

H68593 223 bp mRNA EST 27-OCT-1995
 LOCUS yu69606.r1 Homo sapiens cDNA clone 239074 5' similar to gb:M87789
 DEFINITION IG GAMA-1 CHAIN C REGION (HUMAN);

ACCESSION H68593
 NID 91027333

KEYWORDS EST.
 SOURCE human clone-239074 primer-M13R1 library-Weismann Olfactory

ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 223)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasaks, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE Wash-Merck EST project
 JOURNAL Unpublished (1995)
 COMMENT

REFERENCE 1 (bases 1 to 223)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevasaks, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE Wash-Merck EST project
 JOURNAL Unpublished (1995)
 COMMENT

CONTACT: Wilson RK
 Wash-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Source: IMAGE Consortium, LBNL
 This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbnl.gov) for further information.

FEATURES
 Location/Qualifiers
 1..223

Source
 /organism="Homo sapiens"
 /clone="239074"
 <1..>223
 mRNA
 BASE COUNT 35 a 75 c 66 g 46 t 1 others
 ORIGIN

Query Match 26.7%; Score 144; DB 12; Length 223; Best Local Similarity 93.2%; Pred. No. 7.2e-33; Matches 150; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 376 GCTATGACACTGGGGTCAAGCAGCAGTGTACCGTCTCCACAGCTCCAGAGG 435
 DB 60 GCCTTGACACCTGGGGCCAGGAGACCTGTCTCCGTCTCCACAGCTCCAGAGG 119
 QY 436 CCATGGTCTTCCCGTGGACACCTCTCCAGAGCAGCTGGGGGACAGGCGCTG 495
 DB 120 CCATGGTCTTCCCGTGGACACCTCTCCAGAGCAGCTGGGGGACAGGCGCTG 179
 QY 496 GGCTGCTGTGCAAGAGTACTTCCCGAAGCAGGAGCGT 536
 DB 180 GGCTGCTGTGCAAGAGTACTTCCCGAAGCAGGAGCGT 220

RESULT 15

AA377074 291 bp mRNA EST 21-APR-1997
 LOCUS AA377074
 DEFINITION EST89603 Small intestine I Homo sapiens cDNA 5' end similar to similar to immunoglobulin heavy chain, VDJ regions (GB:214165), mRNA sequence.

ACCESSION AA377074
 NID 92029413

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 291)

REFERENCE 1 (bases 1 to 291)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C., Clifton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Friedman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Heblum, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marra, S.M., Merrick, J.M., Moreno, Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, O.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Yi, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 COMMENT

CONTACT: Kerlavage, AR
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 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavage@igrr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/db/hgi/hgi.html)
 Seq primer: M13 Reverse.

FEATURES
 Location/Qualifiers
 1..291

Source
 /organism="Homo sapiens"
 /note="Organ: small intestine; Vector: pBluescript SK-";
 Site_1: EORI; Site_2: XhoI
 /db_xref="ATCC (inhost):181500"
 /db_xref="taxon:9606"
 /clone_lib="Small intestine I"

MRNA /dev_stage="adult"
BASE COUNT 67 a 73 c 89 g 61 t 1 others
ORIGIN

Query Match 26.5%; Score 143.2; DB 18; Length 291;
Best Local Similarity 69.7%; Pred. No. 1.3e-32;
Matches 193; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGAATGCACCTGGGCTATTCTCTTCTTGGTATCAACAGCTACAGTGTCCACTCCAG 60
DB 15 ATGACTGAGCTGAGATCTCTTCTTGGTGGCAGCAGCTACAAAGTCCCACTCCCA 74
QY 61 GTCCACTAGTGCAGCTGAGGCTGAGGTTAAGAGCCTGGGCTTCAAGTGAAGGTGTC 120
DB 75 GTGCACTGCTGATCTGAGGCTGAGGTTAAGAGCCTGGGCTTCTCTGTGAAAGTTCG 134
QY 121 TGCAGGCTTCTGGCTACACCTTCACAGCTAGTGCATTTGGTGAAGGCGGCT 180
DB 135 TGCAGGCTTATGATACACCTTCACGATATATCACTCACTGAGGCGGCT 194
QY 181 GGCACAGCTAGAGTGTGAGAGATGATCTCTGTGAGAGTAACTAATCACTAAT 240
DB 195 GGACAGGCTTGTGATGATGAGATGAACCAATGAGGCTCCGACTGTGCA 254
QY 241 CAAATATCAAGGAGGCTCAGATGATGAGCA 277
DB 255 CAGAGTTTCGGGGAGAGTCACTCTGACAGGACA 291

Search completed: May 11, 1999, 11:44:16
Job time: 503 sec

GenCore version 4.5
(c) 1993 - 1998 CompuLink

ALIGNMENTS

(without alignments)
1147.790 Million cell updates/sec

Title: US-08-700-737-18

Sequence: 1 ATGAAATGCACCTGGTCA.....CCGAACGGTGACGGTGTCTG 540

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	540	100.0	540	1	V20076	DNA encoding the p
2	379.6	70.3	494	1	V20085	Consensus DNA sequ
3	359.2	66.5	420	1	V20078	DNA encoding murine
4	354.4	65.6	9208	1	065659	Vector conty. TCAR
5	345.4	64.0	428	1	V20089	DNA sequence of m
6	341.4	63.2	750	1	T08482	Chimeric heavy cha
7	334.8	62.0	1389	1	T62931	2A2 (Chimeric) hu
8	334.8	62.0	1392	1	T62932	Murine anti-porcini
9	334.8	62.0	1392	1	T62932	2A2 human g2/g4 c
10	334.8	62.0	5250	1	T62935	2A2 human IgG4 exp
11	334.4	61.9	1395	1	T62935	Murine anti-porcini
12	334.4	61.9	1392	1	T62937	3F4 (Chimeric) hu
13	334.4	61.9	3400	1	T62937	3F4 human g2/g4 c
14	334.4	61.9	5300	1	T62938	3F4 human IgG4 exp
15	332.8	61.6	11529	1	043844	MAb 55.1 heavy cha
16	329.4	61.0	1582	1	094037	MAb 55.1 heavy cha
17	327.8	60.7	762	1	T03381	Anti-IL-8 MAb 664
18	327.8	60.7	762	1	T78555	Chimeric monoclonal
19	327.8	60.7	762	1	T79350	Chimeric monoclonal
20	327.8	60.7	762	1	V03217	Murine variable re
21	327.8	60.7	762	1	V06418	Chimeric monoclonal
22	327.8	60.7	762	1	V10317	Chimeric MAb 664.2
23	323.2	59.9	10704	1	043846	Plasmid pAH4625. A
24	320	59.3	1617	1	035099	Plasmid pAH4625. A
25	319	59.1	750	1	T08483	Antibody D heavy c
26	318.4	59.0	10844	1	043848	Humanised 5G1.1 VH
27	318.4	59.0	142954	1	T40914	Plasmid pAH4808. A
28	318.4	59.0	3282	1	T40914	Nucleotide sequenc
29	318.2	58.9	690	1	T43874	DNA encoding VH re
30	314.2	58.2	750	1	T08487	Anti-HGF receptor
31	310.8	57.6	12132	1	043847	Humanised 5G1.1 VH
32	307.8	57.0	750	1	T08484	Plasmid pAH4807. A
33	306.8	56.8	2399	1	075356	Humanised 5G1.1 VH
34	302	55.9	1553	1	079930	OKT3 monoclonal an
35	301.2	55.8	458	1	015164	anti-tobacco mosai
36	298.4	55.3	4691	1	092547	VH18 region of an
37	298.4	55.3	6166	1	092547	Pcomb3 expression
38	298.4	55.3	687	1	T15202	Expression vector
39	296	54.8	2178	1	025592	PC3AP313 anti-teta
40	291.2	53.9	1458	1	023571	Encodes 4D5 Fab Ig
41	289.6	53.6	1458	1	023581	Reshaped CD4 antili
42	287.6	53.3	1467	1	023570	Reshaped CD4 antili
43	287.6	53.3	11336	1	043497	Reshaped CAMPATR-H-1
						Approximate nucle

44 284.6 52.7 1581 1 048037 Monoclonal antibod
 45 280.2 51.9 1570 1 012637 Monoclonal antibod

ALIGNMENTS

RESULT 1
 V20076 1
 V20076 standard; DNA; 540 BP.

ID V20076; (first entry)
 AC V20076;
 DE DNA encoding the heavy chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MacCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 OS inflammatory bowel disease; ss.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FH Key 1..540
 CDS /tag= a
 /transl_except= (pos: 94..96, aa: Arg)
 /note= "no stop codon given"
 sig_peptide 1..57
 mat_peptide /tag= b
 58..540
 /tag= c

WO9806248-A2.
 19-FEB-1998.
 06-AUG-1997; U13884.
 15-AUG-1996; US-700737.
 (LEUK-) LEUKOSITE INC.
 Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 Saldaña J,
 WPI: 98-159172/14.
 P-PSDB; W53813.
 Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 22, Fig 11; 145pp; English.
 CC The present sequence encodes the heavy chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MacCAM-1, which is present of high endothelial
 CC venules in muscosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 CC Sequence 540 BP; 120 A; 150 C; 150 G; 120 T;

Query Match 100.0%; Score 540; DB 1; Length 540;
 Best Local Similarity 100.0%; Pred. No. 8e-132;
 Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ATGAATGCACCTGGGTCATCTCTCTTGGTATCAACAGCTACAAAGTGCACCTCCAG 60
 Db 1 ATGAATGCACCTGGGTCATCTCTCTTGGTATCAACAGCTACAAAGTGCACCTCCAG 60

61 GTTCAACATAGTGCATCTGGGGCTAGGTTAAGAAGCTGGGGGCTTCAGTAGAGTGTCC 120
 Db 61 GTTCAACATAGTGCATCTGGGGCTAGGTTAAGAAGCTGGGGGCTTCAGTAGAGTGTCC 120

121 TGCAGGGTTCTGGCTACACCTTCACAGCTACTGATGATGGGTGAGGAGCGGCT 180
 Db 121 TGCAGGGTTCTGGCTACACCTTCACAGCTACTGATGATGGGTGAGGAGCGGCT 180

QY 181 GCCCAGCTCTAGAGTGATGAGAGATGATTCCTTCTGAGAGTAATACTACTACAT 240
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 494 BP; 113 A; 120 C; 118 G; 104 T;

QY 361 GACGATGGAGCTATGCTATTGACTACTGGGGTCAAGGACCTGTCACCTCTCTCA 420
 CC
 Db 361 GACGATGGAGCTATGCTATTGACTACTGGGGTCAAGGACCTGTCACCTCTCTCA 420
 CC
 QY 421 GCTCCACCAAGGCGCCATCGCTCTCCCTGACACCTCTCTCAAGACCTCTGGG 480
 CC
 Db 421 GCTCCACCAAGGCGCCATCGCTCTCCCTGACACCTCTCTCAAGACCTCTGGG 480
 CC
 QY 481 GGCACAGCGGCTGGGCTGGCTGGTCAAGGACTACTTCCCGAAGCGGTGACGTCTCG 540
 CC
 Db 481 GGCACAGCGGCTGGGCTGGCTGGTCAAGGACTACTTCCCGAAGCGGTGACGTCTCG 540
 CC

RESULT 2

V20085
 ID V20085 standard; DNA; 494 BP.

DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable heavy chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease; SS.

OS Mus sp.
 FH Key
 FT CDS

Location/Qualifiers
 13..445
 /*tag- a
 /note- "no stop codon given"
 /transl_except- (pos: 16..18, aa: Xaa)
 /transl_except- (pos: 19..21, aa: Xaa)
 /transl_except- (pos: 22..24, aa: Xaa)
 /transl_except- (pos: 25..27, aa: Xaa)
 /transl_except- (pos: 28..30, aa: Xaa)
 /transl_except- (pos: 31..33, aa: Ile)
 /transl_except- (pos: 34..36, aa: Xaa)
 /note- "Xaa- unknown"
 13..69
 sig_peptide
 /*tag- d
 mat_peptide
 70..445
 /*tag- e

NO9806248-A2.
 PD 19-FEB-1998.
 PR 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Seidman J.
 DR WPI; 98-159172/14.
 DR P-PSDB; W53816.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 1; 145pp; English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal

CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 494 BP; 113 A; 120 C; 118 G; 104 T;

Query Match 70.3%; Score 379.6; DB 1; Length 494;
 Best Local Similarity 83.0%; Pred. No. 3,7e-90;
 Matches 399; Conservative 23; Mismatches 59; Indels 0; Gaps 0;

QY 1 ATGAATGACACCTGGGCTATCTCTTCTGATCAACAGCTACAGTCTCCAG 60
 Db 13 ATGRRATGASCTRRKTRCATYCTCTTGTGATCAACAGCTACAGTCTCCAG 72
 QY 61 GTCCACTAGTCAGTCTGGGGCTGAGGTTAAGAGCCTGGGCTTCAAGAGTCTCC 120
 Db 73 GTCCAACTGACAGCCTGGGGCTGAGGTTAAGAGCCTGGGCTTCAAGAGTCTCC 132
 QY 121 TGCAGAGGTTCTGCTACACCTTCAACAGCTACTGATGATGAGGAGCGCCT 180
 Db 133 TGCAGAGGTTATGCTACACCTTCAACAGCTACTGATGATGAGGAGCGCCT 192
 QY 181 GGCACAGCTCTAGAGTGATGAGAGATGATGATCTCTGAGAGTAATACTACTACAT 240
 Db 193 GGCACAGCGCTTGGATGATGAGAGATGATGATCTCTGAGAGTAATACTACTACAT 252
 QY 241 CAAATATCAAGGAGACCGGCTACATGAGTGTGACATTCCTGATACACAGCTTACATG 300
 Db 253 CAAATATCAAGGAGACCGGCTACATGAGTGTGACATTCCTGATACACAGCTTACATG 312
 QY 301 GAGCTCAGACCGCTGAGATCTGAGACACCTCGGCTACTATTGTGCAAGGAGGCTTAC 360
 Db 313 GAGCTCAGACCGCTGAGATCTGAGACACCTCGGCTACTATTGTGCAAGGAGGCTTAC 372
 QY 361 GACGATGGAGCTATGCTATTGACTACTGGGGTCAAGGACCTGTCACCTCTCTCA 420
 Db 373 GACGATGGAGCTATGCTATTGACTACTGGGGTCAAGGACCTGTCACCTCTCTCA 432
 QY 421 GCTCCACCAAGGCGCCATCGCTCTCCCTGACACCTCTCTCAAGACCTCTGGG 480
 Db 433 GCTCCACCAAGGCGCCATCGCTCTCCCTGACACCTCTCTCAAGACCTCTGGG 492
 QY 481 G 481
 Db 493 G 493

RESULT 3

V20078
 ID V20078 standard; DNA; 420 BP.

DT 14-JUL-1998 (first entry)
 DE DNA encoding murine Act-1 heavy chain variable region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease; SS.

OS Mus sp.
 FH Key
 FT CDS

Location/Qualifiers
 1..420
 /*tag- a
 sig_peptide
 1..57
 /*tag- b
 mat_peptide
 58..420

FT 13-NOV-1992; US-978891.
 PN 03-NOV-1993; US-149099.
 PR (IDEC-) IDEC PHARM CORP.
 PI Anderson DR, Hanna N, Leonard JE, Newman RA, Rastetter WH,
 PI Refsme:
 DR WPI: 94-183162/22.
 PT Treating B cell lymphoma with chimeric antibody - against CD20,
 PT causing rapid depletion of peripheral B cells, also new
 PT antibodies and hybridomas
 PS Disclosure: Fig 3; 101pp: English.
 CC The sequence shows a vector contg. rCAE8, a gene encoding a chimeric
 CC anti-CD20 antibody for treatment of B cell lymphomas. rCAE8
 CC contains 4 transcriptional cassettes, human Ig light and heavy chain
 CC constant regions, dihydrofolate reductase, neomycin phosphotransferase
 CC and murine variable regions. The vector can be used to produce
 CC antibodies which cause depletion of peripheral blood B cells,
 CC including those associated with lymphoma. They mediate complement-
 CC dependent lysis and lyse target cells by antibody-dependent cellular
 CC cytotoxicity.
 CC See also 065629-35.
 SQ Sequence 9208 Bp; 2237 A; 2399 C; 2388 G; 2182 T;
 Sequence 420 Bp; 104 A; 106 C; 112 G; 98 T;

Query Match 66.5%; Score 359.2; DB 1; Length 420;
 Best Local Similarity 91.0%; Pred. No. 7.1e-85;
 Matches 382; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGAATGACCTGGGCTGCTCTCTCTGATCAACAGCTCAAGTGTCCAG 60
 DB 1 ATGGGATGAGGCTGATCATCTCTCTGATCAACAGCTCAAGTGTCCAG 60
 QY 61 GTCCAACTAGTCAGTCTGGGGCTGAGTTAGAGCCCTGGGCTCAAGTGTCC 120
 DB 61 GTCCAACTAGTCAGTCTGGGGCTGAGTTAGAGCCCTGGGCTCAAGTGTCC 120
 QY 121 TCGAAGGCTTGGCTGACCTGACCTGACCTGATGATGATGGTGAAGGCGGCT 180
 DB 121 TCGAAGGCTTGGCTGACCTGACCTGACCTGATGATGATGGTGAAGGCGGCT 180
 QY 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 CAAAATTCAGGAGCGCTGACATGATGATGATGATGATGATGATGATGATGAT 300
 DB 241 CAAAATTCAGGAGCGCTGACATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

RESULT 4
 ID 065629 standard; DNA; 9208 Bp.
 AC 065629;
 DT 01-FEB-1995 (first entry)
 DE Vector contg. rCAE 8 DNA.
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;
 OS cell lysis; ss.
 PN 065629-35.
 PD 26-MAY-1994.
 PF 12-NOV-1993; U10953.

QY 13-NOV-1992; US-978891.
 DB 03-NOV-1993; US-149099.
 QY 2400 ATGGGATGAGGCTGATCATCTCTCTGATCAACAGCTCAAGTGTCCAG 2459
 QY 61 GTCCAACTAGTCAGTCTGGGGCTGAGTTAGAGCCCTGGGCTCAAGTGTCC 120
 DB 2460 GTACAACTGACAGGCTGAGGCTGAGTGTGAGGCTGAGGCTGAGTGTCC 2519
 QY 121 TCGAAGGCTTGGCTGACCTGACCTGACCTGATGATGATGGTGAAGGCGGCT 180
 DB 2520 TCGAAGGCTTGGCTGACCTGACCTGATGATGATGGTGAAGGCGGCT 180
 QY 181 GGCACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 2580 GGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2639
 QY 241 CAAAATTCAGGAGCGCTGACATGATGATGATGATGATGATGATGATGATGAT 300
 DB 2640 CAGAATTCAGGAGCGCTGACATGATGATGATGATGATGATGATGATGATGAT 2699
 QY 301 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 2700 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 GAGCTGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 2760 TACGGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 GGCCTCAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 2820 GCTAGCAGGAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 GGCACAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 2880 GGCACAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

RESULT 5
 ID V20089 standard; DNA; 428 Bp.
 AC V20089;
 DT 14-JUL-1998 (first entry)
 DE DNA sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscular atrophy; murine antigen binding region; inhibition;
 KW humanised antibody; murine antigen binding region; inhibition;

KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease; ss.
 OS Mus sp.
 FH Key
 FT CDS
 Location/Qualifiers
 18..428
 /tag= a
 /note= "no stop codon given"

MO9806248-A2.
 PN 19-FEB-1998.
 PD 06-AUG-1997; U13884.
 PF 15-AUG-1996; US-700737.
 PR (LEUK-) LEUKOSTITE INC.
 PA Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 PI MPI; 98-159172/14.
 DR P-PSDB; W53818.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 2; 145pp; English.
 CC The present sequence represents the nucleotide sequence comprising the
 CC variable region of murine Act-1 antibody determined from clone H2B#34.
 CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adhesion
 CC cell adhesion molecule-1 (MacCAM-1) is a ligand of this particular
 CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
 CC to MacCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. The present sequence was used to construct chimeric,
 CC humanised Act-1 antibodies, which contain murine antigen binding-regions
 CC The humanised immunoglobulin can be used to inhibit the interaction of
 CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
 CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
 CC treating inflammatory diseases such as inflammatory bowel disease. The
 CC immunoglobulin can also be used for detection, isolation and diagnosis.
 SQ Sequence 428 BP; 108 A; 104 C; 115 G; 101 T;

Query Match 64.0%; Score 345.4; DB 1; Length 428;
 Best Local Similarity 90.0%; Pred. No. 2.8e-81;
 Matches 370; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 ATGAATGACGCTGGGCTATCTCTTCTGATCAACAGCTCAACAGTCCACCTCCAG 60
 DB ATGGAGGAGCTATATCATCTCTTCTGATCAACAGCTCAACAGTCCACCTCCAG 77
 QY 61 GTCCAACTAGCTAGCTGGGGCTGAGGTTAAGAGCCTGGGGCTTCAAGAGTGCTCC 120
 DB GTCCAACTGACAGCGCTGGGGCTGAGCTGTGAAAGCCTGGAGCTTCAAGAGTGCTCC 137
 QY 121 TGCAGAGGTTCTGGCTACACCTTCACAGCTACTGATGATGGTGAGGAGCGCCT 180
 DB 121 TGCAGAGGTTATGCTTACACCTTCACAGCTACTGATGATGGTGAGGAGCGCCT 197
 QY 138 TGCAGAGGTTATGCTTACACCTTCACAGCTACTGATGATGGTGAGGAGCGCCT 197
 DB 181 GGCCAACTAGCTAGGAGTGGAGATGATGATCTCTGAGAGTATTAATACTAATAAT 240
 QY 198 GGCAAGGCTTGGAGTGGAGATGATGATCTCTGAGAGTATTAATACTAATAAT 257
 DB 241 CAAAATTCAAGGAGCGCTGACATTGACCTGAGACATTTCCGCTACACAGCTACATG 300
 QY 258 CAAAATTCAAGGAGCGCAATTCATGAGACATTTCCGCTACACAGCTACATG 317
 DB 301 GACCTAGCAGCTGAGATGAGAGACATGCGGCTACTATTTGCAAGAGGGGGTTAC 360
 QY 318 CACCTAGCAGCTGAGATGAGAGACATGCGGCTACTATTTGCAAGAGGGGGTTAC 377
 DB 361 GACGAGTGGAGTATGATGATGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 411
 QY 378 GACGAGTGGAGTATGATGATGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 428

RESULT 6
 ID T08482
 AC T08482;
 T08482 standard; DNA; 750 BP.

DT 02-APR-1996 (first entry)
 DE Chimeric heavy chain 5G1.1M1 VL HUG1 DNA.
 KM Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antiinflammatory; antibody engineering;
 KM humanised antibody; complementarity determining region; CDR;
 KW chimeric antibody; Fab; ds.
 OS Synthetic.
 FH Key
 FT CDS
 Location/Qualifiers
 1..750
 /tag= a
 signal_peptide 1..57
 mat_peptide 58..747
 /tag= b
 /tag= c

MO9529697-A1.
 PN 09-NOV-1995.
 PD 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MD, Matis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 PI MPI; 95-392923/50.
 DR P-PSDB; R776609.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Claim 26; Page 116-119; 181pp; English.
 CC A DNA construct (T08481) codes for chimeric light chain 5G1.1M1 VL
 CC Huk (R77608), which can form the light chain portion of an Fd.
 CC The chimeric light chain includes CDRs derived from mouse anti-C5
 CC monoclonal antibody 5G1.1. The DNA can be subcloned with DNA
 CC (T08482) coding for chimeric Fd (R77609) into vector APEX-3P (T08476)
 CC for prodn. of chimeric Fab in human 293 EBNA cells. Such recombinant
 CC antibodies retain the ability of Mab 5G1.1 to block human complement
 CC C5a generation and thus to reduce glomerular inflammation and kidney
 CC dysfunction associated with glomerulonephritis.
 SQ Sequence 750 BP; 174 A; 226 C; 191 G; 159 T;

Query Match 63.2%; Score 341.4; DB 1; Length 750;
 Best Local Similarity 78.1%; Pred. No. 3.5e-80;
 Matches 424; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

1 ATGAATGACGCTGGGCTATCTCTTCTGATCAACAGCTCAACAGTCCACCTCCAG 60
 DB 1 ATGAATGAGCTGGGCTATCTCTTCTGATCAACAGCTCAACAGTCCACCTCCAG 60
 QY 61 GTCCAACTAGCTAGCTGGGGCTGAGGTTAAGAGCCTGGGGCTTCAAGAGTGCTCC 120
 DB 61 GTCCAACTGACAGCGCTGGGGCTGAGCTGTGAAAGCCTGGAGCTTCAAGAGTGCTCC 120
 QY 121 TGCAGAGGTTCTGGCTACACCTTCACAGCTACTGATGATGGTGAGGAGCGCCT 180
 DB 121 TGCAGAGGTTCTGGCTACACCTTCACAGCTACTGATGATGGTGAGGAGCGCCT 180
 QY 181 GGCCAACTAGCTAGGAGTGGAGATGATGATCTCTGAGAGTATTAATACTAATAAT 240
 DB 181 GGCAAGGCTTGGAGTGGAGATGATGATCTCTGAGAGTATTAATACTAATAAT 240
 QY 241 CAAAATTCAAGGAGCGCTGACATTGACCTGAGACATTTCCGCTACACAGCTACATG 300
 DB 241 GAAACCTTCAAGGAGCGCGCATTCATGAGACATTTCCGCTACACAGCTACATG 300
 QY 301 GACCTAGCAGCTGAGATGAGAGACATGCGGCTACTATTTGCAAGAGGGGGTTAC 360
 DB 301 CAACCTAGCAGCTGAGATGAGAGACATGCGGCTACTATTTGCAAGAGGGGGTTAC 360
 QY 361 GACGAGTGGAGTATGATGATGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 417
 DB 361 GGTAGTAGCCCAAGTGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 418 TACGCTCCACCAAGGCGCCATGCTTCCCTCCGACCTCTCTCCAGAGACCTCT 477

Db 421 TCACCTCCACCAAGGGCCATCGCTCTCCCGGCGCCCTCTCCACAGACCACTCT 480
 QY 478 GGGGCGACAGCGCCCTGGGCTGCTGCTGACAGACTACTTCCCGAAGCGGTGACGCTG 537
 Db 481 GGGGCGACAGCGCCCTGGGCTGCTGCTGACAGACTACTTCCCGAAGCGGTGACGCTG 540
 QY 538 TCG 540
 Db 541 TCG 543

RESULT 7

T62931
 ID T62931 standard; cDNA; 1389 BP.
 AC T62931;
 DT 16-JUN-1997 (first entry)
 DE 2A2 (Chimeric) human G2/G4 chimeric antibody cDNA.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 PN MO9711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR P-PSDB; W14933.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosures: Page 42-44; 105pp; English.
 CC A cDNA clone (T62931) codes for a chimeric antibody (W14933)
 CC comprising the C1 and hinge regions of human IgG2 and the C2 and C3
 CC regions of human IgG4 (G2/G4 Mab) and a murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (Mab) 2A2
 CC heavy chain variable region sequence (see also T62930). A 2A2
 CC human G2/G4 expression plasmid insert sequence is provided in
 CC T62932. The chimeric antibody is specific for porcine VCAM. It is
 CC useful for diagnosing human rejection of porcine xenotransplants
 CC and for improving xenotransplantation of porcine cells, tissues and
 CC organs into human recipients.
 SQ Sequence 1389 BP; 324 A; 425 C; 371 G; 269 T;

Query Match 62.0%; Score 334.8; DB 1; Length 1389;

Best Local Similarity 78.0%; Pred. No. 2.1e-78;

Matches 421; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

QY 1 ATGAATGACACCTGGGCTATCTTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
 Db 1 ATGGGATGGAGCTATATCTTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAATAGTACGCTGGGCTGAGGTTAAGAGCTGGGCTTACGTAAGTGTCC 120
 Db 61 GTTCACTGACAGCTGTGGGCTGAGGTTAAGAGCTGGGCTTACGTAAGTGTCC 120
 QY 121 TGCAGAGCTTCTGCTACACCTTCCACAGCTAGTGTGATGGTGGAGCGCCCT 180
 Db 121 TGCAGAGCTTCTGCTATCTTCACTTACCAAGCTATGATGCTGGTGGAGCGCCCT 180
 QY 181 GGCACAGCTAGAGTGGATGCGAAGATGATCTTCTGAGAGTAACTACTACAT 240
 Db 181 GGCACAGCTAGAGTGGATGCGAAGATGATCTTCTGAGAGTAACTACTACAT 240
 QY 241 CAATAATTCAGAGCGGTACATGTAGCTAGCAATTCGCTAGACAGCTTACATG 300
 Db 241 CAGAGGTTAAGGACAGCGCATATGCTGTGACAAATCTCCACACAGCTACATG 300

QY 301 GAGCTCAGACAGCTGAGATGTAGAGACACTGCGGTCTACTATTGTGCAAGAGGGGTTAC 360
 Db 301 CAATTCCAGCGCCGAGACTTGTAGAGACTGCGGTCTATTACTACAAAGAGGG----- 356
 QY 361 GAGGATGGAGACATATGATTAAGTACTGAGGTCACAGGACAGCTGTGACCCCTCTCA 420
 Db 356 -----AGGTTCTGCTGTTGCTTACTGAGGCGAGGGAGCTGTGCTCTGCA 408
 QY 421 GCCTCCACAGAGGCGCCATGCTTCCCGCTGGACACCTCTCTCAAGAGACACTGTGG 480
 Db 409 GCCTCCACAGAGGCGCCATGCTTCCCGCTGGACACCTCTCTCAAGAGACACTGTGG 468
 QY 481 GGCACAGCGCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 469 AGACAGCGCCCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528

RESULT 8

T62930
 ID T62930 standard; DNA; 1392 BP.
 AC T62930;
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 2A2 heavy chain DNA sequence.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Mus sp.
 PN MO9711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI; 97-212855/19.
 DR P-PSDB; W14932.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosures: Page 40-42; 105pp; English.
 CC DNA sequences (T62929-30) respectively code for the light chain
 CC (W14931) and heavy chain (W14932) of murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (Mab)
 CC 2A2. Hybridoma 2A2 was produced by standard techniques using
 CC recombinant, soluble porcine VCAM as immunogen. Chimeric
 CC antibodies can be produced by cloning Mab 2A2 and 3F4 (see also
 CC T62934-35) variable regions into expression plasmid pAPEX-3P
 CC modified to contain the human gamma4 constant region in place of
 CC the human gamma1 C1 region. Sequences are provided for 2A2
 CC (chimeric) human G2/G4 cDNA (T62931), a 2A2 human G2/G4 expression
 CC plasmid insert (T62932), and a 2A2 human IgG4 expression plasmid
 CC insert (T62933). The chimeric antibodies are specific for porcine
 CC VCAM. They are useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 SQ Sequence 1392 BP; 326 A; 421 C; 373 G; 272 T;

Query Match 62.0%; Score 334.8; DB 1; Length 1392;

Best Local Similarity 78.0%; Pred. No. 2.1e-78;

Matches 421; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

QY 1 ATGAATGACACCTGGGCTATCTTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
 Db 1 ATGGGATGGAGCTATATCTTCTTGTGATCAACAGCTACAGTGTCCACTCCAG 60
 QY 61 GTCCAATAGTACGCTGGGCTGAGGTTAAGAGCTGGGCTTACGTAAGTGTCC 120
 Db 61 GTTCACTGACAGCTGTGGGCTGAGGTTAAGAGCTGGGCTTACGTAAGTGTCC 120
 QY 121 TGCAGAGCTTCTGCTACACCTTCCACAGCTAGTGTGATGGTGGAGCGCCCT 180
 Db 121 TGCAGAGCTTCTGCTATCTTCACTTACCAAGCTATGATGCTGGTGGAGCGCCCT 180

Db 121 TGCAGGCTTCGTGTTACTCATTCACGCTATTGATGCATCGGTGAGCAGAGGCT 180
 QY 181 GGGCAAGCTAGAGTGGATGAGAGATTTGATCCTTCGAGAGTAATTAATCAAT 240
 Db 181 GGACAGATCTTGATGATTTGGATGATTTGATTCATTCGATGAGTAATTAAT 240
 QY 241 CAAAATTCAGAGGAGCGGTCACATTGACTAGACATTTCCGTAGCAGACCTACATG 300
 Db 241 CAGAGGTTAAAGGACAGGCGCATTTGACTGTGACAAATCTCCAGACAGCTACATG 300
 QY 301 GAGCTCAGACGCTAGATCTAGACACACTGGGTCTACTATTGTGCAAGAGGGTTAC 360
 Db 301 CAATTACAGCGGCGCCACTCTGAGACCTGCGGTCTATTACTGTACAGAGGG- 356
 QY 361 GACGGATGGAGTATGATGACTAGTGGGGTCAAGGACCGCTGTCACGCTCTCTCA 420
 Db 361 -----AGTTTCTGTTGCTTCTTACTGAGGCGCAGGGGACCTGTCTCTCTCA 408
 QY 421 GCTTCACCAAGGCGCCATCGGTCTTCCCTCGACACCCCTCTCCAGAGACCTTGGG 480
 Db 409 GCTTCACCAAGGCGCCATCGGTCTTCCCTCGACACCCCTCTCTCTCTCTCTCA 468
 QY 481 GGCACAGCGGCGGCTGGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGCGTGC 540
 Db 469 AGCACAGCGGCGGCTGGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGCGTGC 528

RESULT 9

T62932 standard; DNA: 3400 BP.

AC T62932;

DT 16-JUN-1997 (first entry)

DE 2A2 human G2/G4 chimeric antibody expression plasmid insert.

KW xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAM; monoclonal antibody;

KW Chimeric antibody; diagnosis; ss.

OS Chimeric Homo sapiens;

OS Chimeric Mus sp.

FH Key location/Qualifiers

FT exon 903..1055

FT Intron /tag- a

FT Intron /tag- b

FT exon /tag- c

FT Intron /codon_start- 1318

FT Intron /tag- d

FT exon /tag- e

FT Intron /tag- f

FT exon /tag- g

FT Intron /tag- h

FT exon /tag- i

FT Intron /tag- j

FT exon /tag- k

FT Intron /tag- l

FT exon /tag- m

FT Intron /tag- n

FT exon /tag- o

FT Intron /tag- p

FT exon /tag- q

FT Intron /tag- r

FT exon /tag- s

FT Intron /tag- t

FT exon /tag- u

FT Intron /tag- v

FT exon /tag- w

FT Intron /tag- x

FT exon /tag- y

FT Intron /tag- z

FT exon /tag- a

FT Intron /tag- b

FT exon /tag- c

CC T62931) chimeric antibody expression plasmid insert sequence.
 CC The chimeric antibody (W14934) is specific for porcine vascular
 CC cell adhesion molecule (VCAM) and is useful for diagnosing human
 CC rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into
 CC human recipients.
 SQ Sequence 3400 BP; 776 A; 993 C; 899 G; 732 T;

Query Match

Best Local Similarity

Matches 421; Conservative

Score 334.8; DB 1; Length 3400;

Pred. No. 2.0e-78;

Mismatches 107; Indels 12; Gaps 1;

QY 1 ATGAATGACCTGGGCTATCTCTCTGATATCAACAGCTACAGTCCACTCCAG 60
 Db 1318 ATGGATGACCTATATCATCTTCTCTGATATCAACAGCTACAGTCCACTCCAG 1377
 QY 61 GTCCACTAGTGCAGTCTGGGGCTGAGGTTAAGACCTGGGCTTCAGTGAAGTCTC 120
 Db 1378 GTACAACTGCAGACTCTGGGCTCAGCTGAGGCTTGGGCTTCAGTGAAGTATCC 1437
 QY 121 TGCAGGCTTGGCTACCTTCACAGCTAGTGAAGTGAAGTGAAGGAGGAGGCT 180
 Db 1438 TGCAGGCTTGGCTACCTTCACAGCTAGTGAAGTGAAGTGAAGGAGGAGGCT 1497
 QY 181 GGCACAGCTAGAGTGGATGGAGATGATCTCTGAGATTAATTAATTAATTAAT 240
 Db 1498 GGACAGATCTTGAAGTGGATGGATGGATGGATGGATGGATGGATGGATGGAT 1557
 QY 241 CAAAATTCAGAGGAGCGGTCACATTGACTGATGACATTTCCGTAGCAGCCTACATG 300
 Db 1558 CAGAGGTTAAAGGACAAAGGCGCATTTGACTGATGACATTTCCGTAGCAGCCTACATG 1617
 QY 301 GAGCTCAGACGCTGAGATCTGAGACACCTGGGTCTACTTGTGAAGAGGGGGTTAC 360
 Db 1618 CAATTACAGCGGCGCCACTCTGAGACCTGCGGTCTATTACTGTACAGAGGGG- 1673
 QY 361 GACGGATGGAGTATGATGACTAGTGGGTCAAGGACCTGTCACCGCTCTCTCA 420
 Db 1673 -----AGTTTCTGTTGCTTCTTACTGAGGCGCAGGGGACCTGTCTCTCTCA 1725
 QY 421 GCTTCACCAAGGCGCCATCGGTCTTCCCTCGACACCCCTCTCCAGAGCCTTGGG 480
 Db 1726 GCTTCACCAAGGCGCCATCGGTCTTCCCTCGACACCCCTCTCTCTCTCTCTCA 1785
 QY 481 GGCACAGCGGCGGCTGGGTGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGCGTGC 540
 Db 1786 AGCACAGCGGCGGCTGGGTGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGCGTGC 1845

RESULT 10

T62932 standard; DNA: 5250 BP.

AC T62932;

DT 16-JUN-1997 (first entry)

DE 2A2 human IgG4 expression plasmid insert sequence.

KW xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAM; monoclonal antibody;

KW Chimeric antibody; diagnosis; ss.

OS Chimeric Homo sapiens;

OS Chimeric Mus sp.

FH Key location/Qualifiers

FT exon 903..1055

FT Intron /tag- a

FT Intron /tag- b

FT exon /tag- c

FT Intron /tag- d

FT exon /tag- e

FT Intron /tag- f

FT exon /tag- g

FT Intron /tag- h

FT exon /tag- i

FT Intron /tag- j

FT exon /tag- k

Db	1590	CAGAAAGTTCAAGGGCCAAAGGCCACATTGACATCGAGATAAATCCCTCCAGCACACGCTACATG	1649
QY	301	GAGCTTCACAGACCCCTCGAATATCTAGAGACACCTGCGGCTACTATATTGTGCACAAAGGGGGTAC	360
Db	1650	CAACCTCAGCACCCTTGGCATCTGAGAGACTGCGGGTATTATCTGTCCAAAGAGCTGACGTA	1709
QY	361	GACGGATGAGCATATGCTATTGACTACTGAGGGTCAAGGACACCCCTGGTCAACCGCTCTCA	420
Db	1710	GGAGGCT-----ACTTTGACTACTGGGGCCAAAGGACACACCTCTCAACTCTCTCA	1760
QY	421	GCTTCACACAAAGGGCCCATGCGTCTTCCCTCTGGCACCTCTCTCCAAAGACCTCTTGGG	480
Db	1761	GCTTCACACAAAGGGCCCATCGCTCTTCCCTCTGGCCCTCTGCTCCAGAGGACACTCTCCAG	1820
QY	481	GGCACAGGCGCCCTGGGGCTGCTGGTCAAGATACCTTCCCGGAACCGGTGACGGGTGCG	540
Db	1821	AGCACAGCCGCTCTGGGCTGCTGTGTCACAGATCACTTCCCGGAACCGGTGACGGGTGCG	1880

QY 1 MKCTWILFLVSTATSVHSQVLQSGAEVKKPGASVKVSCCKSGYTFSTSYMHHWVRQAP 60

QY 121 DGWDYADYWGQGLTVVSS 140
 DB 118 --WRDAFDIMGQGTMTVSS 135

RESULT 14

PL0011
 Ig heavy chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996

C:Accession: PL0011

R:Cheng, H.L., Sood, A.K., Ward, R.E., Kieber-Emmons, T., Kohler, H.

MOL. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.

A:Reference number: PL0011; MUID:88142863

A:Accession: PL0011

A:Molecule type: mRNA

A:Residues: 1-151 <CHP>

A:Experimental source: cell line 4C11

C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>

F:50-54/Region: complementarity-determining 1

F:69-85/Region: complementarity-determining 2

F:118-125/Region: complementarity-determining 3

F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 53.0%; Score 506; DB 2; Length 151;

Best Local Similarity 64.3%; Pred. No. 5.7e-35;

Matches 99; Conservative 18; Mismatches 31; Indels 6; Gaps 2;

QY 1 MKCTVILFVSTATSVHSGVQLVDSGAEVKKPKGASVYKSCGSGYFTFTSYMMHWYRQAP 60

DB 1 MGSWIFLFLSLGAGVLSVQLQSGPELKPASVYKISCRASGYFTFTSYMMHWYKQSH 60

QY 61 GQRLWIEIDPSESNTNINQKFKGRVTLVDISASTAYMELSLRSEDTAVYYCARGGY 120

DB 61 GKSLEWIGFDPNNTYNEKFKKATLTVDKSSTAYMELSLRSEDSAVYYCA---- 117

QY 121 DGWDYADYWGQGLTVVSSASTKGPSPVPLAP 153

DB 117 -SYDYGALDYWGQGTSTVYSSAKTTPPSVYPLAP 149

RESULT 15

MHMS18

Ig heavy chain precursor V region (B1-8) - mouse

N:Contains: Ig heavy chain precursor V region 186-2

C:Species: Mus musculus (house mouse)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 20-Mar-1998

C:Accession: A90809; B90809; A22069; A02036

R:Botwell, A.L.M.; Paskind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som

A:Reference number: A90809; MUID:81234548

A:Accession: A90809

A:Molecule type: DNA

A:Residues: 1-139 <B18>

A:Cross-references: GB:J00529; NID:9195114; PID:9195115

A:Accession: B90809

A:Molecule type: DNA

A:Residues: 1-117 <1862>

A>Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hap

A>Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA

R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.

EMBO J. 1, 635-640, 1982

A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between

A:Reference number: A90971; MUID:84236026

A:Accession: A22769

A:Molecule type: protein
 A:Residues: 20-139 <DIL>
 A>Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch V of the mu chain

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:118-124/Region: D segment

F:125-139/Region: J segment (JH2)

Query Match 53.0%; Score 505.5; DB 1; Length 139;

Best Local Similarity 70.4%; Pred. No. 5.7e-35;

Matches 95; Conservative 14; Mismatches 25; Indels 1; Gaps 1;

QY 6 VILFVSTATSVHSGVQLVDSGAEVKKPKGASVYKSCGSGYFTFTSYMMHWYRQAPGRLE 65

DB 6 IMLFLAATATGVSQVQLQDPAELVYKPGASVYKLSCKASGYFTFTSYMMHWYKQRRGLE 65

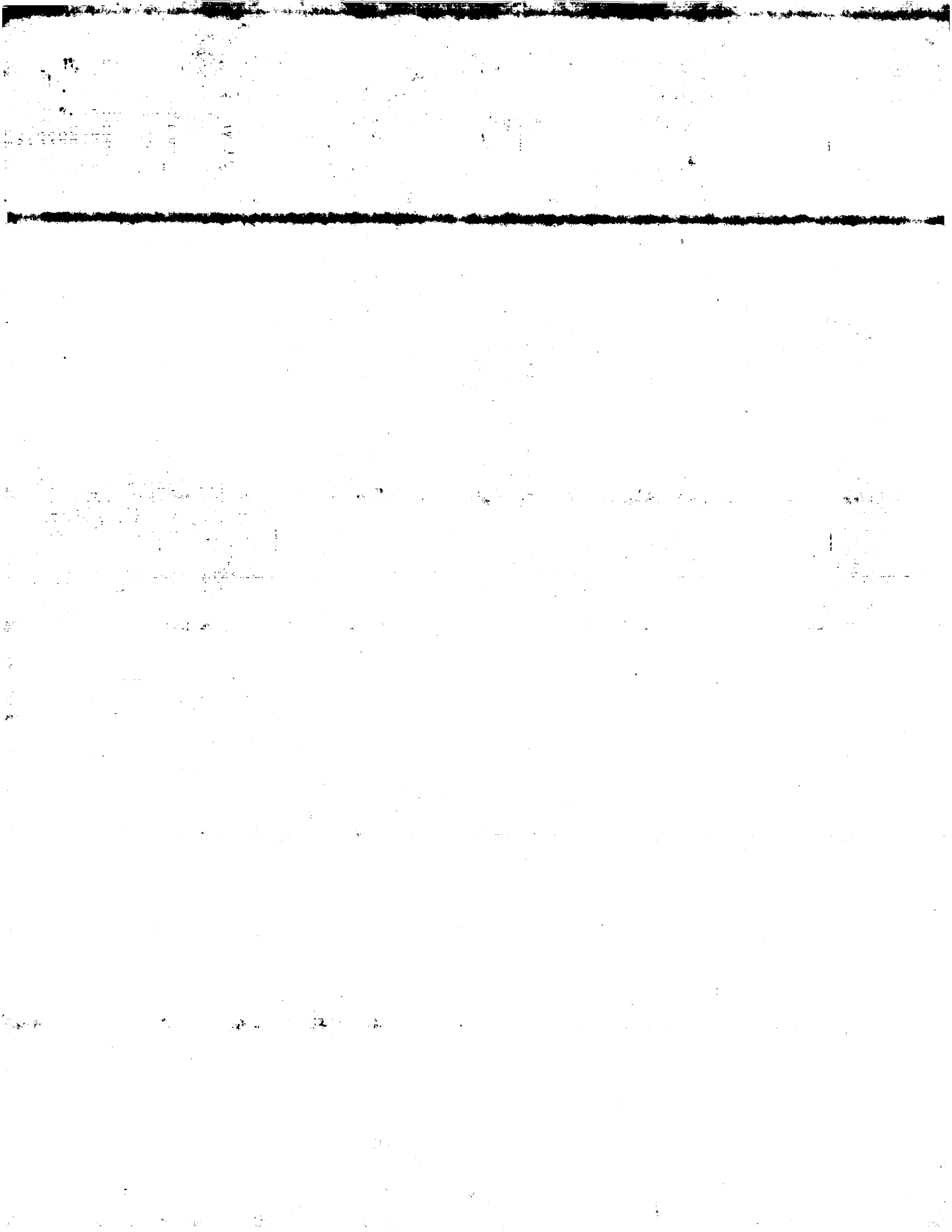
QY 66 WIGELDPSESNTNINQKFKGRVTLVDISASTAYMELSLRSEDTAVYYCARGGYDGDY 125

DB 66 WIGRIDPNSGQTKYKFKKATLTVDKPSTAYMQLSLRSEDSAVYYCARYDYGGSSY 125

QY 126 AIDYWGQGLTVVSS 140

DB 126 -FDYWGQGLTVVSS 139

Search completed: May 11, 1999, 12:23:24
 Job time: 297 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:20:08 ; Search time 22.45 Seconds

(without alignments)
215,201 Million cell updates/sec

Title: US-08-700-737-19

Perfect score: 954
Sequence: 1 MACTWVILFLVSTAFVSHSQ.....GTAALGLVKDYFPEPTVS 180

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database : SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	505.5	53.0	139	1 HV07_MOUSE	P01751 mus musculu
2	491	51.5	138	1 HV48_MOUSE	P03980 mus musculu
3	471	49.4	117	1 HV16_HUMAN	P23083 homo sapien
4	470	49.3	117	1 HV06_MOUSE	P01750 mus musculu
5	467	49.0	140	1 HV02_MOUSE	P01746 mus musculu
6	465.5	48.8	137	1 HV11_MOUSE	P01755 mus musculu
7	455	47.7	117	1 HV18_MOUSE	P01743 homo sapien
8	453.5	47.5	143	1 HV1C_HUMAN	P01744 homo sapien
9	447	46.9	117	1 HV05_MOUSE	P01749 mus musculu
10	445	46.6	117	1 HV09_MOUSE	P01753 mus musculu
11	443	46.4	117	1 HV04_MOUSE	P01748 mus musculu
12	443	46.4	136	1 HV15_MOUSE	P01759 mus musculu
13	437.5	45.9	120	1 HV30_MOUSE	P06329 mus musculu
14	433	45.4	117	1 HV49_MOUSE	P06328 mus musculu
15	427	44.8	117	1 HV10_MOUSE	P01754 mus musculu
16	425	44.5	120	1 HV03_MOUSE	P01747 mus musculu
17	421.5	44.2	118	1 HV51_MOUSE	P06330 mus musculu
18	419	43.9	117	1 HV12_MOUSE	P01756 mus musculu
19	417	43.7	117	1 HV13_MOUSE	P01757 mus musculu
20	414	43.4	117	1 HV14_MOUSE	P01758 mus musculu
21	398	41.7	117	1 HV52_MOUSE	P06337 mus musculu
22	394	41.3	121	1 HV01_MOUSE	P01745 mus musculu
23	366	38.4	117	1 HV1A_HUMAN	P01742 homo sapien
24	363.5	38.1	114	1 HV00_MOUSE	P01741 mus musculu
25	354	37.1	125	1 HV1E_HUMAN	P06336 homo sapien
26	352.5	36.9	136	1 HV16_MOUSE	P01783 mus musculu
27	352	36.9	142	1 HV01_RAT	P01805 rattus norv
28	351.5	36.8	124	1 HV1D_HUMAN	P01760 homo sapien
29	350	36.7	117	1 HV42_MOUSE	P01812 mus musculu
30	347.5	36.4	119	1 HV37_MOUSE	P01807 mus musculu
31	347.5	36.4	119	1 HV38_MOUSE	P01808 mus musculu
32	347	36.4	121	1 HV3J_HUMAN	P01771 homo sapien
33	346.5	36.3	120	1 HV1H_HUMAN	P80421 homo sapien
34	341	35.7	117	1 HV41_MOUSE	P01811 mus musculu
35	339.5	35.6	119	1 HV40_MOUSE	P01810 mus musculu
36	334.5	35.1	122	1 HV3G_HUMAN	P01768 homo sapien
37	333	34.9	118	1 HV39_MOUSE	P01809 mus musculu
38	330.5	34.6	122	1 HV3H_HUMAN	P01769 homo sapien
39	327.5	34.3	124	1 HV1E_HUMAN	P01761 homo sapien
40	327	34.3	123	1 HV25_MOUSE	P01794 mus musculu
41	325.5	34.1	126	1 HV3K_HUMAN	P01772 homo sapien
42	319	33.4	115	1 HV3D_HUMAN	P01765 homo sapien
43	318.5	33.4	116	1 HV3T_HUMAN	P01781 homo sapien

ALIGNMENTS

44 318 33.3 115 1 HV32_MOUSE P01801 mus musculu
45 317.5 33.3 122 1 HV3A_HUMAN P01762 homo sapien

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RESULT 1
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE: 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
  BALTIMORE D.;
  CELL 24:625-637(1981).
RL -1- THE B1-8 MC CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
  ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
  ANTIBODIES).
CC EMBL J00529; GI95115; -.
DR PIR; A02034; MEMS18.
DR HSSP; P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
FT DOMAIN 50 54 FRAMEWORK 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 118 124 FRAMEWORK 3.
FT DOMAIN 125 139 D SEGMENT.
FT DISULFID 41 115 JH2 SEGMENT.
FT NON_TER 139 BY SIMILARITY.
SQ SEQUENCE 139 AA; 15419 MW; DEB3C7DA CRC32;

```

Query Match 53.0%; Score 505.5; DB 1; Length 139;
Best Local Similarity 70.4%; Pred. No. 1.1e-40;
Matches 95; Conservative 14; Mismatches 25; Indels 1; Gaps 1;

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QY 6 VILFIVSTATSVHSGVQVLOVSGAEVKKRPGASVAVSCGSGYFTSYMMHVRQAPQGRLE 65
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 6 IMFPLATATGCVHSOVQLOPGAEVLPKPGASVAVSLSCASYYTTSYMMHVRQAPQGRLE 65
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 66 WIGSIDPESSTNTYNNQKFGKRVTLVDISASTAYMETLSIRSDPTAVYVCARGYDGMWDY 125
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DB 66 WIGSIDPESSTNTYNNQKFGKRVTLVDISASTAYMETLSIRSDPTAVYVCARGYDGMWDY 125
  ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 126 AIDTWGGGTLVTVSS 140
  ::::: ::::: ::::: :::::
DB 126 -FDYWGSGTTLTVSS 139
  ::::: ::::: ::::: :::::

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RESULT 2
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (REL. 02, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84248078.
 RA GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,
 RA TUCKER P.W.,
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).
 DR HSP; P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION (TEPC 1017).
 FT DOMAIN 21 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 128 138 FRAMEWORK 4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; BEF6247B CRC32;

Query Match 51.5%; Score 491; DB 1; Length 138;
 Best Local Similarity 66.0%; Pred. No. 2,4e-39;
 Matches 93; Conservative 21; Mismatches 23; Indels 4; Gaps 2;

QY 1 MKCTWILFLVSTATSVHSOVOLVOSGAEVKKPGASVYVSCSGGYTFTSYMHVWVROAP 60
 DB 1 MGWSYILFLVATADVHSOVOLVOPGALVPGASVOLSCSKAGHTTANWIMHVKQRP 60
 QY 61 GORLEWIGELIDPSESNNTYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCAR-G 119
 DB 61 GGGLEWIGELINPNGRSRNFKKATLVTDKSSSTAYMOLSLTPREFAVYICARSDG 120
 QY 120 YDGMVDYADWGGGTLYTVSS 140
 DB 121 YYDW---FVYWGQGLTVFSA 138

RESULT 3
 HVLG_HUMAN STANDARD; PRT; 117 AA.
 AC P23083;
 DT 01-NOV-1991 (REL. 20, CREATED)
 DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
 DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88296408.
 RA MATSUDA F., LEE K.R., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
 RA OHNO H., FURUKHARA S., HONJO T.,
 RL EMBO J. 7:1047-1051(1988).
 DR EMBL; X07448; -. NOT_ANNOTATED_CDS.
 DR PIR; S00476; HVH035.
 DR HSP; P01810; 1FVB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13009 MW; FFA560D1 CRC32;

Query Match 49.4%; Score 471; DB 1; Length 117;
 Best Local Similarity 76.9%; Pred. No. 1,5e-37;
 Matches 90; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

DB 1 MDWTRILFLVAAATGASHOVOLVOSGAEVKKPGASVYVSCSGGYTFTSYMHVWVROAP 60
 QY 61 GORLEWIGELIDPSESNNTYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCAR 117
 DB 61 GGGLEWIGELINPNGRSRNFKKATLVTDKSSSTAYMOLSLTPREFAVYICAR 117

RESULT 4
 HVO6_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (102).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE; 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
 RA BALTIMORE D.,
 RL CELL. 24:625-637(1981).
 CC -1- THIS GEMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 DR HSP; P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (102).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 FRAMEWORK 3.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;

Query Match 49.3%; Score 470; DB 1; Length 117;
 Best Local Similarity 79.3%; Pred. No. 1,8e-37;
 Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 6 VILFVSTATSVHSOVOLVOSGAEVKKPGASVYVSCSGGYTFTSYMHVWVROAPGORE 65
 DB 6 IILFVATATGAVSHVQLOOPGALVPGASVYVSCSKASGYTFTSYMHVWVROPGGLE 65
 QY 66 WIGLIDPSESNNTYNOKEFGKRVLTVDISASTAYMELSLRSDTAIVYCA 116
 DB 66 WIGLIDPSESNNTYNOKEFGKRVLTVDKSSSTAYMOLSLTSEDSAVYCA 116

RESULT 5
 HVO2_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (9367).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A/J;
 RX MEDLINE; 82152818.
 RA STMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA CAPRA J.D.;

QY 6 VILELVSTATSHSQVLQVQSGAEFYKPGASTKVSCKSGCYTFLPSYMMHWVRQAPQORLE 65

DB 6 IMLFLATATGVHSQVLQVQSGAEFYKPGASTKXLSCKSKSGYTFPSYLMHWNRQPRGLE 65

	RESULT	8		
HVIC	HUMAN			
ID	HVIC_HUMAN	STANDARD;	PRT;	143 AA.
AC	P01744;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	21-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	HC HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUDAROTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EDUTHERIA; PRIMATES. [1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE: 83065234.			
RX	KENTEN J.H., MOUGARD H.V., HOUGHTON M., DERBYSHIRE R.B., VINNEY J., BELL L.O., GOULD H.J.;			
RA	PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982). [2]			
RN	SEQUENCE OF 16-142.			
RP	BENNICH H.H., JOHANSSON S.G.O., VON BAHR-LINDSTROM H.;			
RA	(IN) IMMEDIATE HYPERSENSITIVITY. MODERN CONCEPTS AND DEVELOPMENTS, RL BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).			
OR	-1 THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN. PIR: A02026; EIHUND.			

DR HSSP; P01607; 1F6V.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON CONS 4 5
FT SIGNAL 1 15
FT CHAIN 16 143
FT MOD_RES 16 16
FT DISULFID 37 111
FT CONFLICT 17 17
FT CONFLICT 49 50
FT CONFLICT 63 64
FT CONFLICT 121 121
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 47.5%; Score 453.5; DB 1; Length 143;
Best Local Similarity 62.6%; Pred. No. 8.1e-36;
Matches 87; Conservative 20; Mismatches 25; Indels 7; Gaps 2;

QY 9 FLVSTATSVHSQVLOVSGAEVKRPGASVSKSGSGYFTSYMMHWVROAPGQRLWIG 68
DB 5 FLVLAATFVHSQTLVSGAEVKRPGASVSKSGSGYFTSYMMHWVROAPGQRLWIG 64
QY 69 EIDSESTNTNOKFKGVTLTVDISASTAMELSSRSEPTAYTCAR-----GGYDGM 123
DB 65 WINPNSGGTNTAPRFGQVWTMTKDSASTAYMDLSRSDSAVAYCAKSDPFMSDYNE 124
QY 124 DYA--IDYWGQGLTVTVSS 140
DB 125 DYSTLDVWGQGLTVTVSS 143

RESULT 9
HV05_MOUSE STANDARD; PRT; 117 AA.
ID P01749;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (3).
OS MUS MUSCULUS (MOUSE).
OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR EMBL; J00536; G554035; -
DR PIR; A02031; HVMS3.
DR HSSP; P01810; 1F6V.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 85 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 0F12PC8B CRC32;

Query Match 46.9%; Score 447; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 2.6e-35;
Matches 84; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QY 6 VILFVSTATSVHSQVLOVSGAEVKRPGASVSKSGSGYFTSYMMHWVROAPGQRL 65

DB 6 IILFVATATGVSQVLOVSGAEVLRPGSSVSKLSCASGTYFTSYMMDWKQRPQGLE 65
QY 66 WIGSIDSESTNTNOKFKGVTLTVDISASTAMELSSRSEPTAYTCAR 117
DB 66 WIGNIYDSESTNOKFKDATTLVKSSSTAYMDLSRSDSAVAYCAR 117

RESULT 10
HV09_MOUSE STANDARD; PRT; 117 AA.
ID P01753; P1271;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (186-1).
OS MUS MUSCULUS (MOUSE).
OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
BALTIMORE D.;
RL CELL 24:625-637(1981).
CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
CC THAT COULD ENCODE V REGIONS OF NP8 ANTIBODIES.
DR PIR; B02034; HVMS61.
DR HSSP; P01810; 1F6V.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 85 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; C97683A2 CRC32;

Query Match 46.6%; Score 445; DB 1; Length 117;
Best Local Similarity 72.3%; Pred. No. 4e-35;
Matches 81; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
QY 6 VILFVSTATSVHSQVLOVSGAEVKRPGASVSKSGSGYFTSYMMHWVROAPGQRL 65
DB 6 IMLFATATGVSQVLOVSGAEVLRPGASVSKLSCASGTYFTSYMMHWKQRPQGLE 65
QY 66 WIGSIDSESTNTNOKFKGVTLTVDISASTAMELSSRSEPTAYTCAR 117
DB 66 WIGRIDPNSGGTNTAPRFGQVWTMTKDSASTAYMDLSRSDSAVAYCAR 117

RESULT 11
HV04_MOUSE STANDARD; PRT; 117 AA.
ID P01748;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (23).
OS MUS MUSCULUS (MOUSE).
OC EDUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234548.
RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
BALTIMORE D.;

RL	CELL 24:625-637(1981).
CC	-1 THIS GENE LINE BELONGS TO A SET OF CLOSELY RELATED GENES.
CC	THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR	PIR; A02030; HYMS23.
DR	HSSP; P01810; IJHL.
KM	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 19
FT	CHAIN 20 117 IG HEAVY CHAIN V REGION (23).
FT	DOMAIN 20 49 FRAMEWORK 1.
FT	DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN 55 68 FRAMEWORK 2.
FT	DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN 86 117 FRAMEWORK 3.
FT	DISULEFID 41 115 BY SIMILARITY.
FT	NON_TER 117 117
SO	SEQUENCE 117 AA; 12772 MW; 66B34DIA CRC32;

Query Match	46.48;	Score	443;	DB 1;	Length	117;	
Best Local Similarity	73.28;	Pred.	No. 6.2e-35;				
Matches	82;	Conservative	11;	Mismatches	19;	Gaps	0

[illegible]

RESULT	12	
HV15_MOUSE		
ID	HV15_MOUSE	STANDARD;
AC	P01759.	PRT; 136 AA

CA	21 JUL-1986	(REL. 01, CREATED)	
DT	21 JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)	
DT	01-FEB-1991	(REL. 17, LAST ANNOTATION UPDATE)	
DE	IG HEAVY CHAIN PRECURSOR V REGION (BCL1).		
OS	MUS MUSCULUS (MOUSE).		
OC	EUMAROTOA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE; 82222262.		
RA	KANMP M.R., LIU C.-P., NEWELL N., WARD R.B., TUCKER P.W., STROBER S.,		
RL	BLATNER F.R.;		
RA	PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).		
DR	EMBL; J00494; G195011; -.		
DR	PIR; A02042; HVMSB1.		
DR	HSSP; P01789; ITEL.		
KW	IMMUNOGLOBULIN V REGION; SIGNAL.		
FT	SIGNAL	1	19
FT	CHAIN	20	136
FT	NON_TER	136	135
SO	SEQUENCE	136 AA;	15078 MW; E04F1C7E CRC32;

Query Match	46.4%	Score 443	DB 1	Length 136
Best Local Similarity	63.5%	Pred. No.	7,4e-35	
Matches	87	Conservative	15	Mismatches 27; Indels 8; Gaps 2

Dy
66 WIGTIDSESNNTNOKKRGVTLTVNDISAATAVMETSIISPEDAVVYVAB--GGYGCW 127
Dy
6 VILFVATISVHSVDVLQSGAEVKRKGASAKVSKCKSGGTFTFSYMMHWNRQAPGLE 65
Dy
6 IIFFLVAITGHSVDLQDSGPVEYVRGVSKIKSCSGTFTFDYAMHWKSHANSLE 65

OY 66 WIGELDPSESNNTYNOKFKGRVLTVDISASTAYMELSSLESDIAYYYCAR--GGYDGM 12
||| | : ||||| : || : || : || : ||| |
Db 66 WIGVISTYNGNTSYNOKFKGKATMTVDKSSSTVNHMLARLTSSEDSANDUCARYGN--- 12

DD 08 WIGVSIINGNISINUNKFA
QY 124 DYALDYWGQGLTVSS 1400
||||||| : |||||

Db 123 ---FDYWGQGTTLTVSS 136

RESULT 13	HY50_MOUSE	STANDARD:	PRT:	120 AA.
ID	HY50_MOUSE			
AC	P06329;			
DT	01-JAN-1988 (REL. 06, CREATED)			
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)			
DT	01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN V REGION (AC38 15.3).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	(1)			
RP	SEQUENCE.			
RX	MEDLINE; 84182519.			
RA	DILDROR R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJESWSKY K.;			
RL	EMBO J. 3:517-523(1984).			
DR	PIR; A02037; MHMS15.			
KW	HSSP; P01772; IEGV.			
KW	IMMUNOGLOBULIN V REGION.			
FT	DOMAIN 1 98			
FT	DOMAIN 99 105			
FT	DOMAIN 106 120			
FT	DISULFID 22 96			
FT	NON_TER 120 120			
FT	SEQUENCE 120 AA; 13311 MM; 85EC01BA CRC32;			
Query Match	45.98;	Score 437.5;	DB 1;	Length 120;
Best Local Similarity	67.88;	Freq. No. 2.1e-34;		
Matches 82;	Conservative 12;	Mismatches 26;	Indels 1;	Gaps 1
QY	20 QVQLQSGAEVKKVPSKVSCVSGSGYFTSYMMHWROAPQRLEWIGDIPSESNY 79			
Db	1 QVQLQPTLELVKPPASVNLSCKASGYFTSYMMHWIRNPQGLEIGINPNSGNTY 60			
QY	80 NQKFRGRTLVYDISASTAVNELSLRSEDNAVYYCARGDGMVDYIDWGQGLVTVS 139			
Db	61 NEKFSKATLVYDKSSSATYMLSTPSEDSAVYYCARWDYG-DRYEDVGTGTVTVS 119			
QY	140 S 140			
Db	120 S 120			
RESULT 14	HY49_MOUSE			
ID	HY49_MOUSE	STANDARD:	PRT:	117 AA.
AC	P06328;			
DT	01-JAN-1988 (REL. 06, CREATED)			
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN PRECURSOR V REGION (VH58 B4).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; RODENTIA.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 8509340.			
RA	YANCOPOULOS G.D., ALT F.W.;			
RL	CELL. 40:271-281(1985).			
DR	EMBL; M13788; G466292; -.			
PIR	A02035; MHMSB4.			
HSSP	P01810; IYHL.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT	SIGNAL 1 19			
FT	CHAIN 20 117			
FT	DOMAIN 20 49			
FT	DOMAIN 50 54			
FT	DOMAIN 55 68			
FT	DOMAIN 69 85			
FT	DOMAIN 86 117			
FT	FRAMEWORK 1.			
FT	FRAMEWORK 2.			
FT	FRAMEWORK 3.			

FT DISULEID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA: 12834 MW: 85692FE5 CRC32;

Query Match 45.48; Score 433; DB 1; Length 117;
 Best Local Similarity 70.58; Pred. No. 5.3e-34;
 Matches 79; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 6 VILFLVSTATSVASOVOLVSGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 Db 6 IMFLFATATGVSFVQLOQPGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65

QY 66 WIGELDPSESNITNYNOKFKGRVTLTYDISASTAYMELSLRSEDTAVYYCAR 117
 Db 66 WIGRIDPNSGCTKYNEKFKATLTVDKPSSTAYMOLSLTSEDSAVYYCTR 117

RESULT 15
 HV10_MOUSE STANDARD; PRT; 117 AA.

ID HV10_MOUSE P11270:
 AC P01754; P11270:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (145).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA BOWMELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 CC EMBL: J00533; G554033; -.
 DR PIR: C02034; HYMS45.
 DR HSSP: P01810; 1JHL.
 DR IMMOGLOBULIN V REGION; SIGNAL.
 KW IMMOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION (145).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT NON_TER 117
 SQ SEQUENCE 117 AA: 12921 MW: D9E6B000 CRC32;

Query Match 44.88; Score 427; DB 1; Length 117;
 Best Local Similarity 70.58; Pred. No. 1.9e-33;
 Matches 79; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 6 VILFLVSTATSVASOVOLVSGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65
 Db 6 IMFLFATATGVSFVQLOQPGAEVKKPGASVYVSCGSGTFTSYMMHWVROAPGQRL 65

QY 66 WIGELDPSESNITNYNOKFKGRVTLTYDISASTAYMELSLRSEDTAVYYCAR 117
 Db 66 WIGRIDPNSGCTKYNEKFKATLTVDKPSSTAYMOLSLTSEDSAVYYCTR 117

Search completed: May 11, 1999, 12:20:08
 Job time: 305 sec

GenCore version 4.5
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OM protein - protein search, using sw model

```
Run on:      May 11, 1999, 12:21:01 ; Search time 38.54 Seconds .
              (without alignments)
              257.666 Million cell updates/sec
```

Title: US-08-700-737-19
Perfect score: 954

Sequence: 1 MKCTWILFLVSTATSHQ.....GTALGCLVKDYFPEPTVS 180

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

```

14: sp.archaea:*
13: sp.unclassified:*
12: sp.verebate:*
11: sp.virus:*
10: sp.yodent:*
9: sp.bacteria:*
8: sp.plant:*
7: sp.phage:*
6: sp.organelle:*
5: sp.mhc:*
4: sp.mammal:*
3: sp.invertebrate:*
2: sp.human:*
1: sp.fungi:*
SPTRMBL.8:*

```

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	23.3	82	2	075729	075729 homo sapien
2	212	22.2	76	2	075742	075742 homo sapien
3	211.5	22.2	85	2	075724	075724 homo sapien
4	199	20.9	88	2	075737	075737 homo sapien
5	198.5	20.8	77	2	075726	075726 homo sapien
6	198	20.8	77	2	075730	075730 homo sapien
7	197.5	20.7	78	2	075728	075728 homo sapien
8	194	20.3	86	2	075722	075722 homo sapien
9	194	20.3	77	2	075741	075741 homo sapien
10	191.5	20.1	81	2	075719	075719 homo sapien
11	191	20.0	74	2	075714	075714 homo sapien
12	189.5	19.9	81	2	075734	075734 homo sapien
13	189	19.8	78	2	075723	075723 homo sapien
14	188	19.7	86	2	075740	075740 homo sapien
15	186	19.5	72	2	075738	075738 homo sapien
16	185.5	19.4	81	2	075721	075721 homo sapien
17	184	19.3	80	2	075735	075735 homo sapien
18	181.5	19.0	80	2	075725	075725 homo sapien
19	181.5	19.0	80	2	075727	075727 homo sapien
20	181.5	19.0	79	2	075731	075731 homo sapien
21	177	18.6	82	2	075732	075732 homo sapien
22	172.5	18.1	81	2	075736	075736 homo sapien
23	172	18.0	76	2	075739	075739 homo sapien
24	164	17.2	78	2	075733	075733 homo sapien
25	163.5	17.1	97	2	043743	043743 homo sapien
26	159.5	16.7	75	2	075743	075743 homo sapien
27	155	16.2	45	2	076051	076051 homo sapien
28	154	16.1	78	2	075720	075720 homo sapien
29	150.5	15.8	254	12	Q90557	Q90557 glingimostc

30	138	14.5	64	10	Q61750	Q61750 musciculu
31	137.5	14.4	258	12	Q90559	Q90559 ginglymstoc
32	132	13.8	250	12	Q90569	Q90569 ginglymstoc
33	127	13.3	258	12	Q90556	Q90556 ginglymstoc
34	126	13.2	119	2	Q99589	Q99589 homo sapien
35	123	12.9	268	12	Q90524	Q90524 ginglymstoc
36	121.5	12.7	121	2	Q99600	Q99600 homo sapien
37	120	12.6	265	12	Q90543	Q90543 ginglymstoc
38	117.5	12.3	684	12	Q90544	Q90544 ginglymstoc
39	116	12.2	145	2	Q16237	Q16237 homo sapien
40	114.5	12.0	38	2	Q15224	Q15224 homo sapien
41	112	11.7	237	12	Q90545	Q90545 ginglymstoc
42	111.5	11.7	130	10	P80913	P80913 mus muscicu
43	111	11.6	158	12	Q90531	Q90531 ginglymstoc
44	109	11.4	257	12	Q90536	Q90536 ginglymstoc
45	108	11.3	188	12	Q90528	Q90528 ginglymstoc

ALIGNMENTS

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RESULT      1
075729      ID 075729      PRELIMINARY; PRT; 82 AA.
AC 075729;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA FISCHER M., KUEPERS R.;
RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
RL mutated VH region genes."
RR SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; AJ009526; E1311452; -.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9396 MW; 9063B32A CRC32;

Query Match          23.3%; Score 222; DB 2; Length 82;
Best Local Similarity 49.4%; Pred. No. 1,2e-13;
Matches 41; Conservative 15; Mismatches 23; Indels 4; Gaps 2

QY 51 YWMAVRAPGPGORLEWICEIDPSBSNTNMYNCKFKGRVLTVDISASTAYMELSLRSEDT 110
   | | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 1 YAMSVMRAPGPGGLEWISDAGIDTYAESVKGRFTISRDNRSKNITLYLQNMTTLAAEDT 60
QY 111 AVYYCARGSDG--WDYAIDPW 130
   ||||| : | | | |||
Db 61 AVYTGVKDGVSANSYWDY-FDIW 82

RESULT      2
075742      ID 075742      PRELIMINARY; PRT; 76 AA.
AC 075742;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
```

01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE,
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT)).

ID 075719 PRELIMINARY; PRT; 81 AA.
 AC 075719;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009516; E1311432; -.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9074 MW; 288593C4 CRC32;

Query Match 20.1%; Score 191.5; DB 2; Length 81;
 Best Local Similarity 42.9%; Pred. No. 7.4e-11;
 Matches 36; Conservative 18; Mismatches 25; Indels 5; Gaps 2;

QY 49 TSYNHWYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSE 108
 DB 1 SYSNHWYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSE 60
 QY 109 DTAIVYCA--RGYDGMWDYDAIW 130
 DB 61 DTAIVYCARDRSGSNDW---LDPW 81

RESULT 11
 075744 PRELIMINARY; PRT; 74 AA.
 AC 075744;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009545; E1311484; -.
 FT NON_TER 1 1
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 8541 MW; 46693A8A CRC32;

Query Match 20.0%; Score 191; DB 2; Length 74;
 Best Local Similarity 44.3%; Pred. No. 7.4e-11;
 Matches 35; Conservative 12; Mismatches 26; Indels 6; Gaps 1;

QY 52 WMHWYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSEDTA 111
 DB 2 WMSAARQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSEDTA 61
 QY 112 VYTCARGLWYVYRISDSRINYNADSVKGRFTISDNKNTLYLQMSLRADTAIVY 130
 DB 62 VYTCATG-----PALDLM 74

RESULT 12
 075734 PRELIMINARY; PRT; 81 AA.
 AC 075734;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009531; E1311462; -.
 FT NON_TER 1 1
 FT NON_TER 81 81
 SQ SEQUENCE 81 AA; 9040 MW; 56B4D902 CRC32;

Query Match 19.9%; Score 189.5; DB 2; Length 81;
 Best Local Similarity 44.4%; Pred. No. 1.1e-10;
 Matches 36; Conservative 14; Mismatches 24; Indels 7; Gaps 1;

QY 50 SYNHWYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSE 109
 DB 1 SYSNHWYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSE 60
 QY 110 TAVYTCAR-----GGYDGM 123
 DB 61 TAVYTCARVLNKKYPNDWY 81

RESULT 13
 075723 PRELIMINARY; PRT; 78 AA.
 AC 075723;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human IgA and IgM secreting intestinal plasma cells carry heavily
 mutated VH region genes."
 RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AJ009520; E1311440; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9075 MW; DFEED569 CRC32;

Query Match 19.8%; Score 189; DB 2; Length 78;
 Best Local Similarity 54.0%; Pred. No. 1.2e-10;
 Matches 34; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 55 WYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSEDTAIVY 114
 DB 1 WYRQAPGRLWIGIDPESNTNNOKEKGVTLTVDISASTAYMELSLRSEDTAIVY 60
 QY 115 CAR 117

Db 61 CAR 63

RESULT 14

ID 075740 PRELIMINARY; PRT: 86 AA.

AC 075740; 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

GN VH.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes."

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009539; E1311474; -.

FT NON_TER 1 1

FT NON_TER 86 86

SO SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;

Query Match

19.7% Score 188; DB 2; Length 86;

Best Local Similarity 51.5% Pred. No. 1.7e-10;

Matches 34; Conservative 13; Mismatches 17; Indels 2; Gaps 1;

OY 52 MNWVROAPGQRLWISGIDPSE--SNTNYPQKFKGRVTLVDISASTAYWELSLRSED 109

Db 3 MNWVROAPGKGLWISGIDPSE--SNTNYPQKFKGRVTLVDISASTAYWELSLRSED 109

OY 110 TAVYYC 115

Db 63 TAVYYC 68

RESULT 15

ID 075738

AC 075738; PRELIMINARY; PRT: 72 AA.

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

GN VH.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.;

RT "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes."

RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ009537; E1311470; -.

FT NON_TER 1 1

FT NON_TER 72 72

SO SEQUENCE 72 AA; 8345 MW; E0FB044A CRC32;

Query Match

19.5% Score 186; DB 2; Length 72;

Best Local Similarity 44.9% Pred. No. 2.1e-10;

Matches 35; Conservative 14; Mismatches 21; Indels 8; Gaps 1;

OY 53 MNWVROAPGQRLWISGIDPSE--SNTNYPQKFKGRVTLVDISASTAYWELSLRSED 112

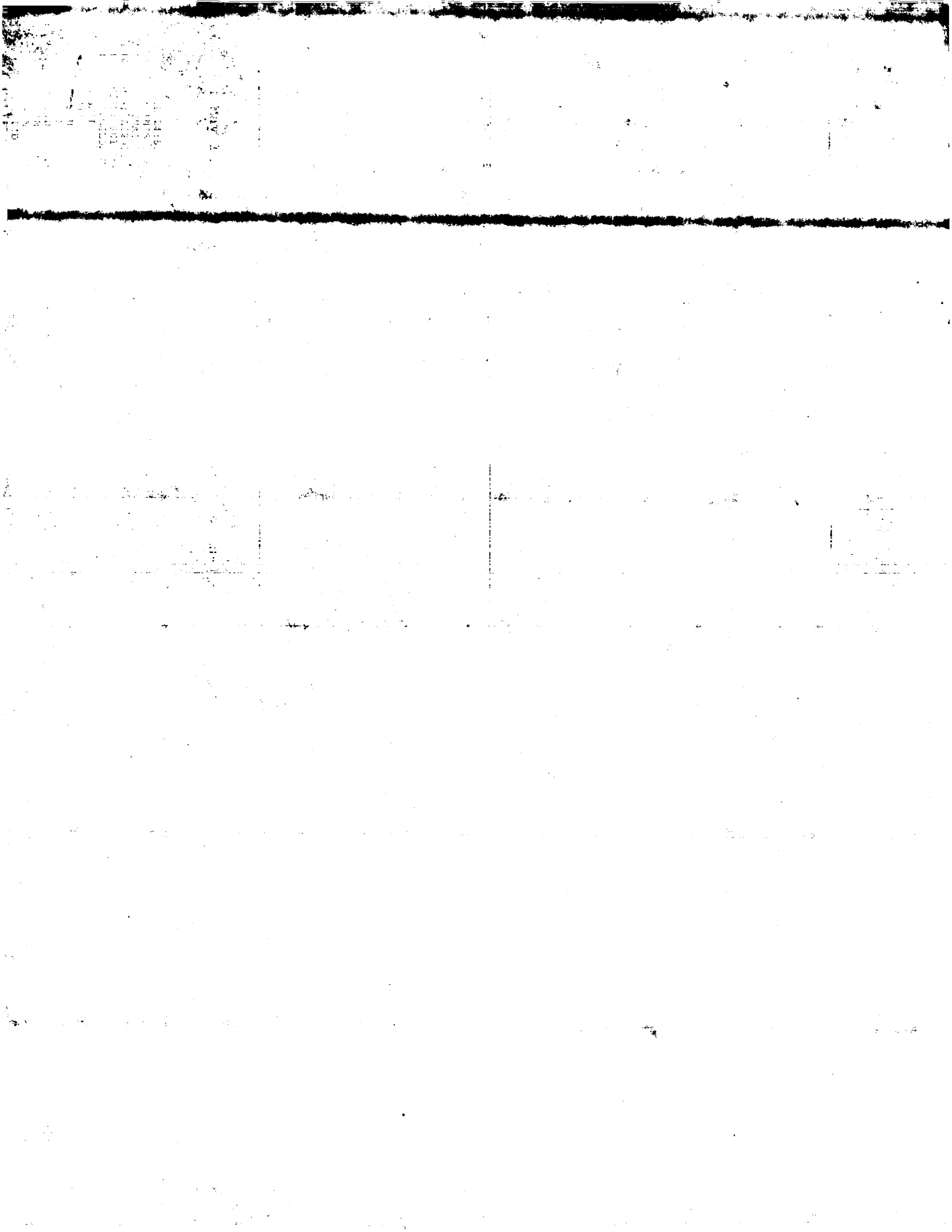
Db 3 MNWVROAPGKGLWISGIDPSE--SNTNYPQKFKGRVTLVDISASTAYWELSLRSED 112

OY 113 YCCARGGSDGMDYALDYW 130

Db 63 YCCARGGSDGMDYALDYW 130

Job time: 253 sec

Search completed: May 11, 1999, 12:21:01



AC R77610; (first entry)
 DE Humanised 5G1.1 VH + IGHRL.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antiinflammatory; antibody engineering;
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 1..19
 FT /label- sig-peptide
 FT 20..249
 FT /label- mat-peptide
 FT region 45..54
 FT /label- CDR-H1
 FT region 69..79
 FT /label- CDR-H2
 FT 118..130
 FT /label- CDR-H3
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR N-PSDB: T08483.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Example 11; Page 119-122; 181pp; English.
 CC A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH
 CC + IGHRL (R77610), includes CDRs derived from mouse anti-C5 monoclonal
 CC antibody 5G1.1. It can be co-expressed with a humanised light
 CC chain (R77612) in human 293 EBNA cells using encoding DNAs
 CC subcloned into vector APEX-3p (T08476). Such humanised recombinant
 CC CDRs retain the ability of Mab 5G1.1 to block human complement
 CC C5a generation and thus to reduce glomerular inflammation and kidney
 CC dysfunction associated with glomerulonephritis.
 SQ Sequence 249 AA;

Query Match 77.28; Score 736.5; DB 1; Length 249;
 Best Local Similarity 78.7%; Pred. No. 2.3e-49;
 Matches 144; Conservative 10; Mismatches 24; Indels 5; Gaps 2;

QY 1 MKCTWVILFLVSTATSVHSQVQLVQSGAEYKRRGASVYVCSKSGYFTSTYMMHWVQAP 60
 DB 1 MKMSWVILFLVSTVAGVHSQVQLVQSGAEYKRRGASVYVCSKSGYFTSNYIOWVQAP 60
 QY 61 GQRLWIGEIDPSESNNTYNNKFKGRVTLVDISASTAYMELSLRSEDVAVYCAR---118
 DB 61 GQGLEWGEIDPSSGSGSTFYAKFGGRVMTADTSTSTAYMELSLRSEDVAVYCARFF 120
 QY 118 GGYGDMYDAIDYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 177
 DB 121 GSSPNWYF--DYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 178
 QY 178 TVS 180
 DB 179 TVS 181

RESULT 3
 ID R77615 standard; Protein; 249 AA.
 AC R77615;
 DE Humanised 5G1.1 VH + IGHRL.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antiinflammatory; antibody engineering;
 OS Synthetic.

FH Key Location/Qualifiers
 FT peptide 1..19
 FT /label- sig-peptide
 FT 20..249
 FT /label- mat-peptide
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; U05688.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR N-PSDB: T08487.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Claim 37; Pages 135-137; 181pp; English.
 CC A DNA construct (T08487) codes for a humanised CDR-grafted
 CC light chain, designated 5G1.1 VL + IGHRLD (R77615), which includes
 CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
 CC DNA can be subcloned together with DNA (T08484) coding
 CC for a humanised Fd (R77611) into vector APEX-3p (T08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 SQ Sequence 249 AA;

Query Match 76.5%; Score 729.5; DB 1; Length 249;
 Best Local Similarity 78.1%; Pred. No. 7.7e-49;
 Matches 143; Conservative 10; Mismatches 25; Indels 5; Gaps 2;

QY 1 MKCTWVILFLVSTATSVHSQVQLVQSGAEYKRRGASVYVCSKSGYFTSTYMMHWVQAP 60
 DB 1 MKMSWVILFLVSTVAGVHSQVQLVQSGAEYKRRGASVYVCSKSGYFTSNYIOWVQAP 60
 QY 61 GQRLWIGEIDPSESNNTYNNKFKGRVTLVDISASTAYMELSLRSEDVAVYCAR---118
 DB 61 GQGLEWGEIDPSSGSGSTFYAKFGGRVMTADTSTSTAYMELSLRSEDVAVYCARFF 120
 QY 118 GGYGDMYDAIDYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 177
 DB 121 GSSPNWYF--DYWGQGLTVVSSASTKGPVFPPLAPSSKSTSGGTALGCLVNDYFPEPV 178
 QY 178 TVS 180
 DB 179 TVS 181

RESULT 4
 ID W48650 standard; Protein; 652 AA.
 AC W48650;
 DE 04-AUG-1998 (first entry)
 KW Heavy chain of hmbp425 fused to TNF alpha.
 KM Antibody-cytokine fusion protein; tristicronic vector; chimeric;
 OS Synthetic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..494
 FT /note- "Heavy chain of human mab 425"
 FT 495..652
 FT /note- "TNF alpha"
 PN WO9811241-A1.
 PD 19-MAR-1998.
 PF 02-SEP-1997; E04765.
 PR 30-SEP-1996; EP-115635.
 PR 16-SEP-1996; EP-114820.
 PA (MERE) MERCK PATENT GMBH.

PI Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C,
 PI Rieke E, von Hoegen I, Welge T;
 DR WPI; 98-207400/18.
 DR N-PSDB; V18096.
 PT Oligo:clstronic expression vector - useful for production of, e.g.
 PS Mab425/TNF- α or Mab425/IL-2 antibody fusion protein
 CC Disclosure; Fig 15; 89pp; English.
 CC The present sequence represents a fusion protein comprising of TNF
 CC alpha fused to the C-terminus of the heavy chain of the human
 CC monoclonal antibody 425 (hmb425). The hmb425 has specificity for
 CC the human EGF receptor. The invention claims for a new pMCDHAP
 CC tricistronic vector (V18096) for the expression of an antibody-cytokine
 CC fusion protein, hmb425-TNF alpha. The TNF alpha sequence can be
 CC substituted by the IL-2 sequence. The vector also contains a strong
 CC promoter/enhancer unit, a selection marker gene and at least two
 CC poliovirus derived internal ribosomal entry site (IRES) sequences. The
 CC vector can be expressed in mammalian host cells for the production of
 CC heteromeric fusion proteins. This expression system is claimed to
 CC produce the heteromeric proteins in high yields.
 SQ Sequence 652 AA;

Query Match 76.2%; Score 727; DB 1; Length 652;

Best Local Similarity 70.1%; Pred. No. 3.2e-48; Mismatches 28; Indels 24; Gaps 1;

Matches 143; Conservative 9; Mismatches 28; Indels 24; Gaps 1;

QY 1 MCKTWLFLVSTATSHVSOVLQVSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 Db 1 MDWTRVFCLLAVAPGASQVQLVQSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 QY 61 GQRLWIGELIDPSESNNTNOKERGVTLTVDISASTAYMELSLRSEDTAVYYCAR 120
 Db 61 GQGLEWIGELIDPSESNNTNOKERGVTLTVDISASTAYMELSLRSEDTAVYYCAR 120
 QY 121 DGMWDYALDYGQGLTVVSS-----ASRKGPEVPELAPSSK 156
 Db 121 DYGRFYDYGQGLTVVSSGEMILCAWQOLCPPRSHGTTSLAATKGPSEVLAPSSK 180
 QY 157 STSGTALGCLVKDYPEPEPTVS 180
 Db 181 STSGTALGCLVKDYPEPEPTVS 204

RESULT 5
 ID R77611 standard: Protein; 249 AA.

AC R77611:
 DT 02-APR-1996 (first entry)
 DE Humanised 561.1 VH + IGHRLC.
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antiinflammatory; antibody engineering;
 OS humanised antibody; complementarity determining region; CDR.
 FH Synthetic.
 FT key Location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT 20..249
 FT /label= mat_peptide
 PN WO9529697-A1.
 PD 09-NOV-1995.
 PF 01-MAY-1995; 005668.
 PR 02-MAY-1994; US-236208.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinco SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 DR N-PSDB; T08484.
 DR WPI; 95-392923/50.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 PS Claim 38; Page 123-125; 181pp; English.
 CC A DNA construct (T08483) codes for a humanised CDR-grafted and
 CC framework sequence-altered Fd 561.1 VH + IGHRL (R77610), which

CC Includes CDRs derived from mouse anti-C5 monoclonal antibody 561.1.
 CC The DNA can be subcloned together with DNA (T08484) coding for a
 CC humanised light chain (R77612) into vector APEX-3P (T08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 561.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 CC Sequence 249 AA;

Query Match 75.5%; Score 720.5; DB 1; Length 249;

Best Local Similarity 77.0%; Pred. No. 3.7e-48; Mismatches 27; Indels 5; Gaps 2;

Matches 141; Conservative 10; Mismatches 27; Indels 5; Gaps 2;

QY 1 MCKTWLFLVSTATSHVSOVLQVSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 Db 1 MKSWLFLVSTATSHVSOVLQVSGAEVKKPGASVKSCKSGYFTSYMMHWQAP 60
 QY 61 GQRLWIGELIDPSESNNTNOKERGVTLTVDISASTAYMELSLRSEDTAVYYCAR 118
 Db 61 GQGLEWIGELIDPSESNNTNOKERGVTLTVDISASTAYMELSLRSEDTAVYYCAR 120
 QY 118 GQIDWDYALDYGQGLTVVSSASTKGPSEVPELAPSSKSTSGTALGCLVKDYPEPV 177
 Db 121 GSSPNWYF--DVGQGLTVVSSASTKGPSEVPELAPSSKSTSGTALGCLVKDYPEPV 178
 QY 178 TVS 180
 Db 179 TVS 181

RESULT 6

R24442
 ID R24442 standard: Protein; 481 AA.

AC R24442;
 DT 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 308
 FT /label= N
 FT /note= "Substn. to create glycan addition site"
 FT misc_difference 310
 FT /label= S
 FT /note= "see above"
 FT misc_difference 321
 FT /label= N
 FT /note= "see above"
 FT misc_difference 329
 FT /label= N
 FT /note= "see above"
 FT misc_difference 331
 FT /label= S
 FT /note= "see above"
 FT misc_difference 356
 FT /label= N
 FT /note= "see above"
 FT misc_difference 369
 FT /label= N
 FT /note= "see above"
 PN WO9209293-A.
 PD 11-JUN-1992.
 PF 18-NOV-1991; 008605.
 PR 23-NOV-1990; US-618314.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Seed B, Walz G;
 DR N-PSDB; Q25443.
 DR WPI; 92-216789/26.
 PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 PT - used in treating chronic inflammation, rheumatoid arthritis,
 PT psoriasis, etc.

PS Disclosure; Fig 1; 46pp; English.
 CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of sialyl-Lex side chains (see R2442, Fig). The
 CC additional N-linked glycosylation sites are introduced at locations
 CC which impair complement fixing and Fc receptor binding ability. They
 CC are preferably located in the CH2 region of the Ig molecule.
 CC Antibodies bearing multiple sialyl-Lex determinants are useful for
 CC disrupting undesirable interactions between cells or proteins.
 CC Disrupting this interaction has therapeutic applications, for
 CC example, in minimizing inflammation following tissue injury.
 SQ Sequence 481 AA;

Query Match 71.9%; Score 685.5; DB 1; Length 481;
 Best Local Similarity 74.7%; Pred. No. 3.3e-45;
 Matches 142; Conservative 9; Mismatches 26; Indels 13; Gaps 4;
 QY 1 MKCTW-VILELVSTATSVHSGVQLVQSGAEYKKRPGASVKSCCKSGYTFSTSYMMHWRAQ 59
 DB 5 MDWTFRLFVVAATGVQSQVLVQSGAEYKKRPGASVKSCCKASGGSFSSYATISWROA 64
 QY 60 PGQLEKIGEDPSESNTNNGKRGRTLVNDISASTAVMELSLRSEDAVYTCAR-- 118
 DB 65 PGQGLEWGGIPIFGTANAKQKFGRTYTADESTSTAYMELSLRSEDAVYTCARDN 124
 QY 118 ----GG--YDGMVDAIDYWGQGLTVYSSASTKGPVFPPLAPSSKSTSGGTALGCLVK 170
 DB 125 GAYSGSGSCISGWM---FDPMGQGLTVYSSASTKGPVFPPLAPSSKSTSGGTALGCLVK 181
 QY 171 DYPEPPTVS 180
 DB 182 DYPEPPTVS 191

RESULT 7
 W05826
 ID W05826 standard; Protein: 279 AA.
 AC W05826;
 DT 27-JAN-1997 (first entry)
 DE Humanised M291 antibody heavy chain.
 KW CD3 antigen; humanised antibody; bispecific antibody;
 KW B-cell lymphoma; myeloma; leukaemia; hybridoma;
 OS Chimeric Homo sapiens;
 FH Key location/Qualifiers
 FT domain 1..120
 FT region /label= variable-domain
 FT region 31..35
 FT region /label= CDR1
 FT region 50..66
 FT region /label= CDR2
 FT region 79..109
 FT region /label= CDR3
 FT misc-difference 30
 FT /note= "human framework residue 30 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 44
 FT /note= "human framework residue 44 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 67
 FT /note= "human framework residue 67 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 68
 FT /note= "human framework residue 68 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 70
 FT /note= "human framework residue 70 is subst. by
 FT equivalent murine framework residue"
 FT misc-difference 72
 FT /note= "human framework residue 72 is subst. by
 FT equivalent murine framework residue"

FT misc-difference 74
 FT /note= "human framework residue 74 is subst. by
 FT equivalent murine framework residue"
 FT domain 121..218
 FT /label= CH1_domain
 FT domain 219..238
 FT /label= Hinge_domain
 FT domain 239..279
 FT /label= Fc-1eucine zipper
 W0626964-A1.
 PD 06-SEP-1996.
 PF 29-FEB-1996; U02754.
 PR 01-MAR-1995; US-397411.
 PA (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
 PI (PROT-) PROTEIN DESIGN LABS INC.
 DR Gingrich R, Link BK, Tso JY, Weiner G;
 WPI: 96-412742/41.
 PT New bispecific antibody reactive with both T or NK cells and
 PT malignant B cells - also their humanised forms and hybridomas
 PT producing them, useful for treating or preventing leukaemia,
 PT lymphoma and myeloma
 PS Claim 28; Fig 5d; 85pp; English.
 CC The humanised M291 antibody heavy chain (W05826) includes a
 CC variable region (see also W05825) consisting of human HF2-1/17
 CC heavy chain variable region framework and complementarily
 CC determining regions from the murine M291 antibody specific for CD3
 CC antigen. It can be coexpressed with humanised M291 light chain (see
 CC also W05830) in mammalian host cells. Bispecific antibodies can
 CC be constructed that include a first binding fragment comprising
 CC humanised M291 heavy and light chain variable regions, and a second
 CC binding fragment comprising humanised ID10 heavy and light chain
 CC variable regions (see also W05828-29). Such antibodies are reactive
 CC with both T or NK cells and malignant B cells, and have therapeutic
 CC and diagnostic aplns.
 SQ Sequence 279 AA;

Query Match 71.2%; Score 679.5; DB 1; Length 279;
 Best Local Similarity 83.3%; Pred. No. 5.5e-45;
 Matches 135; Conservative 5; Mismatches 19; Indels 3; Gaps 2;
 QY 20 QVQLVQSGAEYKKRPGASVKSCCKSGYTFSTSYMMHWRAQPGQLEWGGIPIFGTANAKQK 79
 DB 1 QVQLVQSGAEYKKRPGASVKSCCKASGTYTFSTSYMMHWRAQPGQLEWGGIPIFGTANAKQK 60
 QY 80 NQKFKRGRTLVNDISASTAVMELSLRSEDAVYTCAR--YDGMVDAIDYWGQGLTVY 138
 DB 61 NQKFKRGRTLVNDISASTAVMELSLRSEDAVYTCARSAV--YDGMVDAIDYWGQGLTVY 118
 QY 139 SSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYPEPPTVS 180
 DB 119 SSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYPEPPTVS 160
 RESULT 8
 R43339
 ID R43339 standard; Protein: 449 AA.
 AC R43339;
 DT 29-NOV-1993 (first entry)
 DE Completely humanised C4G1 Ig heavy chain.
 KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
 KW monoclonal antibody; platelet aggregation; humanised antibody.
 OS Synthetic.
 PN W09313133-A.
 PD 08-JUL-1993.
 PF 15-DEC-1992; J01630.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.
 PI Co MS, Tso JY;
 WPI: 93-227275/28.

KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from
 PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 PS Claim 4; Fig 5D; 35pp; English.
 CC This is the amino acid sequence of the humanised antibody C4G1 heavy
 CC chain, used in the method of the invention involving the creation
 CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
 CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
 CC platelet aggregation and also the releasing reaction of platelets. The
 CC Ig can be used for treating cardiovascular diseases and thromboembolic
 CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
 CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
 CC diagnosing the presence and location of a thrombus, or certain types of
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
 CC detection of GPIIb/IIIa antigens or for isolating platelets.
 SQ Sequence 449 AA;

Query Match 70.9%; Score 676; DB 1; Length 449;
 Best Local Similarity 82.8%; Pred. No. 1.6e-44;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAGQLMEIGELDPESSTNTY 79
 DB 1 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAGQLMEIGELDPESSTNTY 60
 QY 80 NQKRGRTLVDSASAVAMELSLRSEDAVAVYCAR--GGYGMWDYADYMGQGLTVT 137
 DB 61 NEKRGRTLVDSSTNAIWEELSLRSEDAVAVFCARRDQNT--GW---FAIYMGQGLTVT 116
 QY 138 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVTS 180
 DB 117 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVTS 159

RESULT 12
 ID W49817
 AC W49817 standard; Protein; 222 AA.
 DT 24-SEP-1998 (first entry)
 DE Fragment of humanised antibody C4G1 heavy chain.
 KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
 KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from

PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 PS Disclosure; Fig 7C; 35pp; English.
 CC This is the amino acid sequence of a fragment of humanised antibody
 CC C4G1 heavy chain, used in the method of the invention involving the
 CC creation of a humanised immunoglobulin (Ig) derived from the mouse
 CC C4G1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa
 CC and inhibiting platelet aggregation and also the releasing reaction of
 CC platelets. The Ig can be used for treating cardiovascular diseases and
 CC thromboembolic disorders, e.g. acute myocardial infarction, unstable
 CC angina, stroke, transient ischemic episodes, deep vein thrombosis and
 CC pulmonary embolism, extracorporeal cardiopulmonary circulation. The
 CC Ig can also be used in diagnosing the presence and location of a
 CC thrombus, or certain types of cancer cells which develop GPIIb/IIIa on
 CC their surfaces, for the detection of GPIIb/IIIa antigens or for
 CC isolating platelets.
 SQ Sequence 222 AA;

Query Match 70.9%; Score 676; DB 1; Length 222;
 Best Local Similarity 82.8%; Pred. No. 8e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

QY 20 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAGQLMEIGELDPESSTNTY 79
 DB 1 QVQLVSGAEYKRRGASVYKSCSGSTFTSYMMHWRAQAGQLMEIGELDPESSTNTY 60
 QY 80 NQKRGRTLVDSASAVAMELSLRSEDAVAVYCAR--GGYGMWDYADYMGQGLTVT 137
 DB 61 NEKRGRTLVDSSTNAIWEELSLRSEDAVAVFCARRDQNT--GW---FAIYMGQGLTVT 116
 QY 138 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVTS 180
 DB 117 VSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYFPEPTVTS 159

RESULT 13
 ID W49818
 AC W49818 standard; Protein; 235 AA.
 DT 24-SEP-1998 (first entry)
 DE Amino acid sequence of a recombinant humanised antibody C4G1 heavy chain.
 KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
 KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
 KW thromboembolic disorder; cancer; acute myocardial infarction;
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PN US5777085-A.
 PD 07-JUL-1998.
 PF 17-MAY-1995; 458516.
 PR 03-MAY-1993; US-053159.
 PR 20-DEC-1991; US-812111.
 PR 09-JUN-1992; US-895952.
 PR 11-SEP-1992; US-944159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Tso JY;
 DR WPI; 98-398136/34.
 PT New humanised immunoglobulin which binds GPIIb/IIIa - derived from
 PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
 PT treating cardiovascular and thromboembolic disorders.
 PS Disclosure; Fig 7D; 35pp; English.
 CC This is the amino acid sequence of a fragment of a recombinant
 CC humanised antibody C4G1 heavy chain, used in the method of the
 CC invention involving the creation of a humanised immunoglobulin (Ig)
 CC derived from the mouse C4G1 antibody. The humanised Ig is capable of
 CC binding to GPIIb/IIIa and inhibiting platelet aggregation and also the
 CC releasing reaction of platelets. The Ig can be used for treating
 CC cardiovascular diseases and thromboembolic disorders, e.g. acute
 CC myocardial infarction, unstable angina, stroke, transient ischemic
 CC episodes, deep vein thrombosis and pulmonary embolism, extracorporeal
 CC cardiopulmonary circulation. The Ig can also be used in diagnosing

CC the presence and location of a thrombus, or certain types of cancer
 CC cells which develop GPIIb/IIIa on their surfaces, for the detection of
 CC GPIIb/IIIa antigens or for isolating platelets.
 SQ Sequence 235 AA;

Query Match 70.9%; Score 676; DB 1; Length 235;
 Best Local Similarity 82.8%; Pred. No. 8.5e-45;
 Matches 135; Conservative 6; Mismatches 16; Indels 6; Gaps 3;

OY 20 QVOLVQSGAEVKKPGASVSVCKSGSYTSTSYMHHVROAPQORLEMGIDPSBSNTNY 79
 DB 1 QVOLVQSGAEVKKPGASVSVCKSGASGIAFTNLIEMVROAPQOGLEMGITPSSGNTNY 60
 OY 80 NQKFKGRVTLTVDISASTAYMELSLRSEDPVAYYCAR--GGYDGMVDYADYWGQGLTVT 137
 DB 61 NEKFKGRVTLTVDESTNAYMELSLRSEDPVAYYFCARDGNY--GM---FAWGGGLTVT 116
 OY 138 VSSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVS 180
 DB 117 VSSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPVTVS 159

RESULT 14

R28808 R28808 standard; Protein; 468 AA.

AC R28808:
 DT 02-APR-1993 (first entry)
 DE pre-5A8 humanised heavy chain
 KW Vector: pMDR1002; NotI; HindIII; pMDR1001; PSAB132; PBAG101; E. coli;
 KW J4221(Iq); ampicillin; resistance; immunoglobulin; signal sequence;
 KW humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
 KW HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
 KW lymphocytes; helper; inducer; HIV; syncytia; formation.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Peptide 1..19
 FT /note="Immunoglobulin signal peptide"
 FT region 20..141
 FT /note="Humanised 5A8 HV"
 FT region 142..468
 FT /note="Human IgG4 HC"

FT WO9209305-A.
 FN 11-JUN-1992.
 PD 27-NOV-1991; U08843.
 PR 27-NOV-1990; US-618542.
 PA (BROJ) BIOGEN INC.
 PI Burkiy LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
 DR N-PSDB: Q30910.
 PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 PS Disclosure: Page 135-56; 205pp; English.
 CC This sequence is encoded by the insert of the vector pMDR1002. Three
 CC fragments were used in the construction of pMDR1002; a 443 bp NotI/
 CC HindIII fragment of pMDR1001 (see Q30905), the 7913 bp NotI linearised
 CC pSAB132 (see Q30906) and a 2109 bp NotI/HindIII fragment of PBAG101
 CC (see Q30909). These fragments were ligated together and the ligation
 CC mixture was used to transform E. coli J4221(Iq) to ampicillin
 CC resistance. This sequence represents the immunoglobulin signal
 CC sequence, amino acids (AA) 1-122 of the humanised 5A8 heavy chain.
 CC variable region (HV) and AA114-AA478 of the human IgG4 heavy chain,
 CC ie, the constant region (HC). This polypeptide is an antibody homolog
 CC which was shown to bind to CD4 but did not block the binding of gp120
 CC to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes
 CC (helper/inducer cells). The homolog blocked HIV-induced syncytia
 CC formation. This homolog can be used in the detection, prophylaxis
 CC and treatment of diseases caused by infective agents whose primary
 CC targets are CD4+ cells.
 SQ Sequence 468 AA;

Query Match 70.3%; Score 670.5; DB 1; Length 468;
 Best Local Similarity 72.3%; Pred. No. 4.5e-44;
 Matches 133; Conservative 16; Mismatches 28; Indels 7; Gaps 2;

OY 1 MKCTWVILFLVSTANVSQVQVQVQSGAEVKKPGASVSVCKSGSYTSTSYMHHVROAP 60
 DB 1 KMTWVRFCLLVAPGASQVQVQVQSGAEVKKPGASVSVCKSGASGTYTSTVIHVRAP 60
 OY 61 GORLEWGEIDPSESNTNYNOKFKGRVTLTVDISASTAYMELSLRSEDPVAYYCARGGY 120
 DB 61 GCGLEWIGIYDYNNGTGYDEKFKKATVTLDPSTNAYMELSLRSEDPVAYYCAR--- 118
 OY 121 DGMVDA---IDYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEP 176
 DB 118 EKDNVATGAMPAYWQGLTVTVSSASTKGPVFPPLAPSSKSTSESTALGCLVKDYFPEP 177
 OY 177 TVVS 180
 DB 178 TVVS 181

RESULT 15

W14941 W14941 standard; Protein; 464 AA.

AC W14941:
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (heavy chain).
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 OS Mus sp.

PN WO97111971-A1.
 PD 03-APR-1997.
 PR 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Mattis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR WPI: 97-212855/19.
 DR N-PSDB: T62938.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure: Page 62-64; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 464 AA;

Query Match 70.2%; Score 669.5; DB 1; Length 464;
 Best Local Similarity 70.5%; Pred. No. 5.3e-44;
 Matches 129; Conservative 17; Mismatches 28; Indels 9; Gaps 2;

OY 1 MKCTWVILFLVSTANVSQVQVQVQSGAEVKKPGASVSVCKSGSYTSTSYMHHVROAP 60
 DB 1 MKMSVILFLVSVTAGVSHQVQVQVQSGAEVKKPGASVSVCKSGASGTYTSTVIHVRAP 60
 OY 61 GORLEWGEIDPSESNTNYNOKFKGRVTLTVDISASTAYMELSLRSEDPVAYYCAR--- 118
 DB 61 GCGLEWIGIATPGGDDSTYQKFKGKATVTLDKSSSTAYMQLSSLASDSNAVYCARTV 120
 OY 118 GGYDGMVDYADYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEP 177
 DB 121 GGY-----FDYWGQGLTVTVSSASTKGPVFPPLAPSSKSTSESTALGCLVKDYFPEP 174

Tue May 11 13:50:11 1999

us-08-700-737-19.rag

Page 8

Oy 178 rvs 180
|||
Db 175 rvs 177

Search completed: May 11, 1999, 12:14:57
Job time: 2104 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 12:00:33 ; Search time 962.98 Seconds

(without alignments)
1534.328 Million cell updates/sec

Title: US-08-700-737-20

Perfect score: 413
Sequence: 1 ATGAAGTGCCTGTTAGGCT.....AAACGGCGTGAATCGCGGCC 413

Scoring table: IDENTITY_NUC

Searched: 808301 segs, 1788773984 residues

Database: GenBank:*

1: gb_ba1:*
2: gb_ba2:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl1:*
9: gb_pl2:*
10: gb_pl3:*
11: gb_pl4:*
12: gb_pl5:*
13: gb_pl6:*
14: gb_pl7:*
15: gb_pl8:*
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39: gb_pl32:*
40: gb_pl33:*
41: gb_pl34:*
42: gb_pl35:*
43: gb_pl36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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1	340	82.3	396	13	MMU16688	U16688 Mus musculus
2	327.2	79.2	396	13	MUSIGKBN	M15874 Mouse Ig ac
3	312.2	75.6	417	13	MMU62051	U62051 Mus musculus
4	308.8	74.8	538	13	MMIGVK	X00045 Mouse mRNA
5	308.2	74.6	538	13	MUSIGKAT	K00709 Mouse Ig ka
6	305.8	74.0	456	13	MMU39901	U39901 Mus musculus
7	302.6	73.3	436	13	MMU012556	AJ012556 Mus muscu
8	300.2	72.7	432	13	MMU62054	U62054 Mus musculus
9	299.4	72.5	432	13	MMU62054	U62054 Mus musculus
10	299	72.4	339	13	MUSIGKCOL	M24275 Mouse Ig ge
11	297.2	72.0	404	13	RAFIGCD2L	M87786 Rat (hybrid
12	294.6	71.3	956	13	MMKAPL1	X87231 M.musculus
13	294.6	71.3	421	13	MMY17589	Y17589 Mus musculus
14	294.2	71.2	805	13	MUSIGKIDH	L12156 W3129; Mus
15	293.6	71.1	416	13	MUSIGKICL	M20828 Mouse IgG2a
16	292	70.7	426	13	MUSIGVK	M55313 Mouse Igr p
17	291.4	70.6	394	6	AR022601	AR022601 Sequence
18	289.2	70.0	351	13	MMU22904	U22904 Mus musculus
19	288.8	69.9	393	13	AF045491	AF045491 Mus muscu
20	288.2	69.8	420	13	S82491	S82491 Tg10 kappa-
21	288.2	69.8	957	13	MMU65535	U65535 Mus musculus
22	288	69.7	336	13	MMIGG2AK	X74588 M.musculus
23	287.2	69.5	393	13	MUSIGK313A	L38105 Mus musculus
24	286.6	69.4	394	6	AR022385	AR022385 Sequence
25	286.6	69.4	394	13	S67233	S67233 IG3VL-muc1
26	286.2	69.3	339	13	MUSIGKCOI	M24272 Mouse Ig ge
27	286.2	69.3	339	13	MUSIGKCOK	M24272 Mouse Ig ge
28	286.2	69.3	323	13	MUSIGKAPD	M64152 Mus musculus
29	286.2	69.3	323	13	MUSIGKAPM	M64161 Mus musculus
30	286	69.2	427	6	A25561	A25561 H.sapiens B
31	286	69.2	427	6	I26967	I26967 Sequence 8
32	285.6	69.2	393	13	AF013576	AF013576 Mus muscu
33	285.6	69.2	393	13	MUSIGK24A	M32382 Mus musculus
34	284	68.8	434	6	A25576	A25576 M.musculus
35	284	68.8	434	6	I26965	I26965 Sequence 4
36	284	68.8	393	13	MUSIGK514	L39088 Mus musculus
37	284	68.8	393	13	MUSIGK940A	L39104 Mus musculus
38	284	68.8	393	13	MUSIGK1240	M32384 Mus musculus
39	283.4	68.6	394	6	AR022571	AR022571 Sequence
40	282.4	68.4	393	13	AF045490	AF045490 Mus muscu
41	282.4	68.4	393	13	MUSIGK1025	M32381 Mus musculus
42	281.2	68.1	384	6	AR013851	AR013851 Sequence
43	280.8	68.0	393	13	AF045494	AF045494 Mus muscu
44	280.8	68.0	393	13	MUSIGK4420	L39087 Mus musculus
45	280.8	68.0	420	13	MMLB41LEV	X65775 M.musculus

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL
1	MMU16688	Mus musculus Ig light chain leader and variable region Vx II gene family mRNA, partial cds.	U16688	91041798	house mouse.	Mus musculus	house mouse.	1 (bases 1 to 396)	White,K.D., Frank,M.B., Foundling,S. and Waxman,F.J.	Effect of immunoglobulin variable region structure on C3b and C4b deposition	Mol. Immunol. 33 (9), 759-768 (1996)	96406984	2 (bases 1 to 396)	Frank,B.	Direct Submission	Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology

RESULT	2
MUSIGKBN	
LOCUS	396 bp mRNA
DEFINITION	Mouse Ig active kappa chain V-J5-C mRNA, from myeloma W3129
ACCESSION	(anti-alpha(1->6)dextran).
NID	M15874
KEYWORDS	g158839
	C-region; J-region; V-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene; variable region subgroup

RESULT	3
LOCUS	MMU62051
DEFINITION	MMU62051 417 bp mRNA ROD 19-FEB-1997 Mus musculus polyreactive autoantibody, immunoglobulin light chain kappa mRNA, partial cds.

ACCESSION U62051
NID 91438582
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 417)
AUTHORS Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.
TITLE Structural and affinity studies of Igm polyclonal natural autoantibodies
JOURNAL J. Immunol. 158 (2), 968-976 (1997)
MEDLINE 97146071
REFERENCE 2 (bases 1 to 417)
AUTHORS Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunopathologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France

FEATURES
source location/Qualifiers
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/organism="Mus musculus"
/strain="N2B"
/note="hybridoma A9A7; 6-day-old spleen cells fused with X63.653 line"
/db_xref="taxon:10090"
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CDS
97 a 99 c 105 g 116 t

BASE COUNT 97 a 99 c 105 g 116 t

ORIGIN

Query Match 75.6%; Score 312.2; DB 13; Length 417;
Best Local Similarity 86.4%; Pred. No. 6.1e-93;
Matches 357; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTTCTGATTCCTGTTCCGGAGT 60
Db 1 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTTCTGATTCCTGTTCCGGAGT 57
QY 61 GATGTTGTGATGACTCAAGTCCACTGCTGCTGCTGACCCCTGAGAACAGCTTCT 120
Db 58 GATGTTGTGATGACTCAAGTCCACTGCTGCTGCTGACCCCTGAGAACAGCTTCT 117
QY 121 ATCTCTTGACAGTCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACTTATTGCTTGG 180
Db 118 ATCTCTTGACAGTCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACTTATTGCTTGG 177
QY 181 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCCTCATCTATGGGATTTCACAGATT 240
Db 178 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCCTCATCTATGGGATTTCACAGATT 237
QY 241 TCTGGGGTGCAGACAGGTTCAAGTTCAGGAGTTCAGGAGATTCACACTCAAGATC 300
Db 238 TCTGGGGTGCAGACAGGTTCAAGTTCAGGAGTTCAGGAGATTCACACTCAAGATC 297
QY 301 TCGGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 360
Db 298 AGCAGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 357
QY 361 TACACGTTCCGACAGGAGCAAGTGTGAATAAAGGGGCTGATGGGGCC 413
Db 358 TTCACGTTCCGACAGGAGCAAGTGTGAATAAAGGGGCTGATGGCC 410

RESULT 4
NMIGVK 538 bp RNA ROD 29-OCT-1996
LOCUS Mouse mRNA for anti-GAT antibody. (poly Glu-60 Ala-30 Tyr-10 random terpolymer).
DEFINITION X00045 K00709
ACCESSION 952532
NID 952532
KEYWORDS Ig kappa light chain; immunoglobulin; signal peptide.
SOURCE house mouse
ORGANISM Mus musculus
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 538)
AUTHORS Schiff, C., Corbet, S., Millil, M. and Fougereau, M.
TITLE Interstrain conservation of the murine GAT-specific antibody V kappa repertoire as analyzed at the germline gene level
JOURNAL EMBO J. 2 (10), 1771-1776 (1983)
MEDLINE 84057697
COMMENT Data kindly reviewed (09-MAY-1985) by M. Fougereau.

FEATURES
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/db_xref="taxon:10090"
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132..188
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132..>538
V_region
/note="variable region joining segment (538 is 2nd base in codon)"
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/codon_start=1
/db_xref="PID:952533"
/translation="MKLPVRLVILFWIPASSSDVYMTOTPLSPVSLGDOASISCS SSVLSHNGNTLYLWYLOKRGOSPKLITRVSNRFGVDPDRSGSGDTFTLNISRY EADDMGVYCFQGHVPHRTFGSGTKLEIKRADAPV"

BASE COUNT 127 a 133 c 132 g 143 t 3 others

ORIGIN

Query Match 74.8%; Score 308.8; DB 13; Length 538;
Best Local Similarity 86.1%; Pred. No. 8.5e-92;
Matches 333; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

QY 1 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTTCTGATTCCTGTTCCGGAGT 60
Db 132 ATGAAGTGGCTGTAGGCTGTGGTCTGTGTTCTGATTCCTGTTCCGGAGT 188
QY 61 GATGTTGTGATGACTCAAGTCCACTGCTGCTGCTGACCCCTGAGAACAGCTTCT 120
Db 189 GATGTTGTGATGACTCAAGTCCACTGCTGCTGCTGACCCCTGAGAACAGCTTCT 248
QY 121 ATCTCTTGACAGTCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACTTATTGCTTGG 180
Db 118 ATCTCTTGACAGTCTAGTCAGAGTCTTGCAAGAGTTATGGGAACACTTATTGCTTGG 177
QY 181 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCCTCATCTATGGGATTTCACAGATT 240
Db 249 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCCTCATCTATGGGATTTCACAGATT 308
QY 241 TCTGGGGTGCAGACAGGTTCAAGTTCAGGAGTTCAGGAGATTCACACTCAAGATC 300
Db 309 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCCTCATCTATGGGATTTCACAGATT 368
QY 301 TCGGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 360
Db 369 TCGGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 428
QY 429 AGCAGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 360
Db 429 AGCAGAGTAGAGGCTGAGAGTGTATTAATCTCTTACCAAGTACACATCAGCCG 360
QY 361 TACACGTTCCGACAGGAGCAAGTGTGAATAAAGGGGCTGATGGCC 410

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Db      489  CACAGGTTCCGAGGGGACCAAGCTGGAATAAATACGGCTGATGCTGC 538
|||||
RESULT  5
MUSIGKAT 538 bp mRNA ROD 01-MAY-1984
LOCUS     Mouse Ig kappa active anti-GAT L XIX 27 V-J region mRNA.
DEFINITION
ACCESSION K00709
KEYWORDS  C-region; J-region; V-region; complementarity determining region;
           framework region; hypervariable region; immunoglobulin light chain;
           immunoglobulin-kappa; processed gene.
SOURCE    Mouse cDNA to hybridoma G8 Ca 1.7 (BALB/c spleen cells fused with
           myeloma cell line X63 Ag8 653) mRNA, clone L XIX 27.
ORGANISM  Mus musculus
           Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae;
           Murinae; Mus.
REFERENCE 1 (bases 1 to 538)
AUTHORS  Schiff, C., Corbet, S., Millil, M. and Fougereau, M.
TITLE     Interstrain conservation of the murine GAT-specific antibody
           V-kappa repertoire as analysed at the germline level
JOURNAL   EMBO J. 2, 1771-1776 (1983)
MEDLINE   84057697
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           source          1..538
                           /organism="Mus musculus"
                           /db_xref="taxon:10090"
BASE COUNT 127 a 133 c 133 g 143 t 2 others
ORIGIN
Query Match 74.6%; Score 308.2; DB 13; Length 538;
Best Local Similarity 86.1%; Pred. No. 1.3e-91;
Matches 353; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

QY      1  ATGAAGTTCCTGTAGGCTGTGGTCTGTTGTTCTGTGATTCTGTTCGGAGGT 60
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Db      132  ATGAAGTTCCTGTAGGCTGTGGTCTGTTGTTCTGTGATTCTGTTCGGAGGT 188
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QY      61  GATGTTGATGATCAACAAAGTCCACTCTCCCTGCTGCACCCCTGGAGAACACTTCT 120
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Db      189  GATGTTGATGATCAACAAAGTCCACTCTCCCTGCTGCACCCCTGGAGAACACTTCT 248
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QY      121  ATCTCTGACAGTCTAGTCAGAGTCTTGTCAAAAGATTAGGGAACCACTATTGTCTGG 180
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QY      181  TACCTGCAGAAAGCCCTGGCCAGTCTCCACAGCTCTCATCTATGAGATTCCAAAGATT 240
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QY      241  TCTGGGGTCCAGACAGTTCAAGTTCAGTGGCAGTGGTTAGGAGACAGATTTCACACTCAAGTC 300
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Db      369  TCTGGGGTCCAGACAGTTCAAGTTCAGTGGCAGTGGTTAGGAGACAGATTTCACACTCAAGTC 428
      |||

QY      301  TCGCAGTAGAGAGCTGAGAGAGCTGGAGTGTATTACTGCTTACAGAGTACACATCAGCCG 360
      |||
Db      429  AGCAGAGTGGAGAGCTGAGAGATATGGAGATTATTTACTGCTTCAAGGTACACATTTCTCT 488
      |||

QY      361  TACAGGTTCCGACAGGAGGACCAAGGTGGAATAAATACGGGCTGATGCGGC 410
      |||
Db      489  CACAGGTTCCGAGAGGAGGACCAAGGTGGAATAAATACGGGCTGATGCTGC 538
      |||

RESULT  6
LOCUS     MMU039901 456 bp mRNA ROD 22-NOV-1996
DEFINITION Mus musculus anti-glycoprotein-B of human Cytomegalovirus
LOCUS     Immunglobulin VI chain mRNA, partial cds.
ACCESSION U39901
NID       91680670

```

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KEYWORDS house mouse.
SOURCE    Mus musculus
ORGANISM  Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
           Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
           Mus.
REFERENCE 1 (bases 1 to 456)
AUTHORS  Schoppel, K., Hassfurth, E., Britz, W., Ohlin, M., Borrebaeck, C.A.
           and Mach, M.
TITLE     Antibodies specific for the antigenic domain 1 of glycoprotein B
           (gp155) of human cytomegalovirus bind to different substructures
JOURNAL   Virology 216 (1), 133-145 (1996)
MEDLINE   96187797
REFERENCE 2 (bases 1 to 456)
AUTHORS  Schoppel, K.
TITLE     Direct Submission
JOURNAL   Submitted (02-NOV-1995) Michael Mach, Institute of Virology,
           University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen,
           Germany
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ORIGIN
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Best Local Similarity 85.5%; Pred. No. 8.1e-91;
Matches 353; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

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QY      61  GATGTTGATGATCAACAAAGTCCACTCTCCCTGCTGCACCCCTGGAGAACACTTCT 120
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QY      121  ATCTCTGACAGTCTAGTCAGAGTCTTGTCAAAAGATTAGGGAACCACTATTGTCTGG 180
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Db      118  ATCTCTGACAGTCTAGTCAGAGTCTTGTCAAAAGATTAGGGAACCACTATTGTGAATGG 177
      |||

QY      181  TACCTGCAGAAAGCCCTGGCCAGTCTCCACAGCTCTCATCTATGAGATTTCACAGATT 240
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Db      178  TACCTGCAGAAAGCCCTGGCCAGTCTCCACAGCTCTCATCTATGAGATTTCACAGATT 237
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QY      241  TCTGGGGTCCAGACAGTTCAAGTTCAGTGGCAGTGGTTAGGAGACAGATTTCACACTCAAGTC 300
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Db      238  TCTGGGGTCCAGACAGTTCAAGTTCAGTGGCAGTGGTTAGGAGACAGATTTCACACTCAAGTC 297
      |||

QY      301  TCGCAGTAGAGAGCTGAGAGAGCTGGAGTGTATTACTGCTTACAGAGTACACATCAGCCG 360
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Db      298  AGCAGAGTGGAGAGCTGAGAGATATGGAGATTATTTACTGCTTCAAGGTACACATGTTCCG 357
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QY      361  TACAGGTTCCGACAGGAGGACCAAGGTGGAATAAATACGGGCTGATGCGGCC 413
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Db      358  TATAGGTTCCGATCGGGGACCAAGCTGGAATAAATACGGGCTGATGCTGCACC 410
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RESULT  7
LOCUS     MMU012556 436 bp mRNA ROD 11-NOV-1998

```


DEFINITION Mus musculus mRNA for H3 specific immunoglobulin, kappa chain, variable region, partial.
ACCESSION AJ012556
NID 93860516
KEYWORDS immunoglobulin superfamily; kappa chain; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 436)
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Wrigley, N.G., Brown, E.B., Daniels, R.S., Douglas, A.R., Skehel, J.J. and Wiley, D.C.
Election microscopy of influenza haemagglutinin-monoconal antibody complexes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 436)
AUTHORS Daniels, R.S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1998) Daniels R.S., Virology Division, National Institute for Medical Research, The Ridgeway, Mill Hill, London, NW7 1AA, UK
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Best Local Similarity 85.0%; Pred. No. 9.3e-90;
Matches 351; Conservative 0; Mismatches 59; Indels 3; Gaps 1;
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58 GATGTTGTGATGACTCAAGTCCACTCTCCCTGCTGACCCCTGGAGAACCACTTCT 117
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118 ATCTCTTGAGGCTTATCTAGAGTCTTGCAAGAGTTATGGAAACACCTATTGTTCTGG 177
QY 181 TACTCGAGAGGCTGGCCAGTCTCCACAGTCTCTCATCTATGGAGTTTCCACAGATT 240
178 TACTCGAGAGGCTGGCCAGTCTCCACAGTCTCTCATCTATGGAGTTTCCACAGATT 237
Db 241 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAAGATC 300
238 TCTGGGGTCCAGACAGGTTCAAGTGGAGTGGTTCAGGAGACAGATTTCACACTCAAGATC 297
QY 301 TCGGAGATTAAGGCTGGAGGAGTGGAGTATATGCTTACAAAGTATACATCAAGCCG 360
298 AGCAGAGTGAAGGCTGGAGGAGTGGAGTATATGCTTCTCAAAATACACATGTTCCG 357

QY 361 TACACGTTCCGAGAGGGACCAAGTGGAAATATAAAGGGCTGATGGCGCC 413
Db 358 TACACGTTCCGAGAGGGACCAAGTGGAAATATAAAGGGCTGATGGCGCC 410
RESULT 8
HS001812 387 bp mRNA ROD 30-MAR-1998
LOCUS
DEFINITION Mus musculus partial mRNA sequence for immunoglobulin light chain V-region (clone 2C7/K18F).
ACCESSION AJ001812
NID 93004453
KEYWORDS immunoglobulin; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 387)
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Mcelyeen, J., Clark, M.R., Smith, S.J., Sewell, H.F. and Shakh, F.
Primary sequence and molecular model of the variable region of a mouse monoclonal anti-der P I antibody showing the same epitope specificity as human Ige. Production of a mouse monoclonal anti-Idiotypic that recognises a cross-reactive idiotype on human Ige
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 387)
AUTHORS Clark, M.R.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-1997) Clark M.R., Pathology Department, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK
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Matches 330; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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Db	253	TCGTGGGTCGCCAGACAGGTTCACTAGTCGACAGTGTTCAGGAGACAGATTTCACACTCAAGATC	312
QY	301	TCGCGAGTGAAGAGGCTGAGAGAGCTGGGAGTGTATTAAGTCTTACAAAGTACATCAGGAC	360
Db	313	AGCAAGTGTGAAGGCTGAGAGTCTGGGAGTGTATTAAGTCTTACAAAGTACATCAGTTC	372
QY	361	TACACGTCGACAGACAGGAGGACCAAGGTGGAATAAAGGCGGTGATCGCGCC	413
Db	373	TTACAGCTTCGGCTCGCGGACCAAAAGTTGGAATAAAGGCGGTGATCGTGCAC	425
RESULT	10		
MUSICCOL			
LOCUS	MUSIGRCOL	339 bp	mRNA
DEFINITION	Mouse Ig germ-line Q52 kappa-chain mRNA (V-J2), partial cds.		
ACCESSION	M24275		
KEYWORDS	9197085		
SOURCE	C-region; J-region; germ-line; immunoglobulin light chain; immunoglobulin-kappa variable region; processed gene.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphia; Muridae; Mus.		
AUTHORS	1 (bases 1 to 339)		
TITLE	Matsuda,T. and Kabat,E.A.		
JOURNAL	Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1---6)dextran		
MEDLINE	J. Immunol. 142 (3), 863-870 (1989)		
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Matches 314;	Conservative 0;	Mismatches 25;	Indels 0;
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RESULT 11			
RATIGCD2L			
LOCUS	RATIGCD2L	404 bp	mRNA
DEFINITION	Rat (hybridoma YTH655) immunoglobulin light chain variable region,	ROD	18-FEB-1993
ACCESSION	complementarity-determining regions mRNA, partial cds.		
KEYWORDS	M87786		
NCBI	g204705		
SOURCE	V-region; complementarity determining region; Immunoglobulin; light chain.		
ORGANISM	Rattus rattus cDNA to mRNA.		
REFERENCE	Rattus rattus		
AUTHORS	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrate; Euthera; Rodentia; Sciurognathi; Myomorphia; Muridae;		
JOURNAL	Murinae; Rattus.		
FEATURES	1 (bases 1 to 404)		
SOURCE	Shearin, J., Walsh, L., Waldmann, H. and Crowe, J.S.		
	Unpublished (1992)		
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Qy 121	ATCTCTTCAGGTCTATGTCACAGTCTTTCGAAAGATTTATGGACACCTATTTCCTGG		180			
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Qy 181	TACCGCAGAAAGCCGGGAGCTGCTCCACAGCTCCCATCTATATGGATTTCCACAGATTT		240			
Db 195	TACCGCAGAAAGCCGGGAGCTGCTCCACAGCTCCCATCTATATGGATTTCCACAGATTT		254			
Qy 241	TCTGGGTGCCAGACAGCTTCAAGTGGCAGTGGTTCGAGGACAGATTTTCACTCAAGATC		300			
Db 255	TCTGGGTGCCAGACAGCTTCAAGTGGCAGTGGTTCGAGGACAGATTTTCACTCAAGATC		314			
Qy 301	TTCGAGTAGAGGCTGAGAGAGCTGGGAGTGTATTACTCTTACCAAGTACACATCAGCCG		360			
Db 315	AGCAGAGTAGAGGCTGAGAGAGCTGGGAGTGTATTACTCTTACCAAGTACACATTTCCG		374			
Qy 361	TACACGTCGGACAGGGGACCAAGGTGAA		390			
Db 375	TACACGTCGGACAGGGGACCAAGGTGAA		404			
RESULT 12						
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DEFINITION	M.musculus mRNA for antibody light chain.					
ACCSSION	X87231					
NID	9854316					
KEYWORDS	C-region; J-region; kappa light chain; V-region.					
SOURCE	house mouse.					
ORGANISM	Mus musculus Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclurognathi; Myomorpha; Muridae Murinae; Mus.					
REFERENCE	1 (bases 1 to 956) Liu,D.H., Guo,J., Chen,S.F., Liang,H. and Wang,H.Y. Cloning and sequencing of kappa light chain gene of a mouse monoclonal antibody directed against potato virus Y (1n) Xiong,J. and Lin,S. (Eds.); GENETIC ENGINEERING AND CROP IMPROVEMENT: 179-188; Huazhong Agricultural University Press, Wuhan, China (1994) 2 (bases 1 to 956) Liu,D.H. Direct Submission Submitted (15-MAY-1995) D.H. Liu, Biotechnology Research Center, Chinese Academy of Agricultural Sciences, 30 Balaishigao Road, Beijing 100081, PROC					
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ORIGIN						

Db	743	TGCTTACAAAGTTTCAATCAGACCGCTCCGCTTCGCTGCTGGAGACCAAGCTGAGCTGAAA	802
QY	397	CGG 399	
Db	803	CGG 805	
RESULT 15			
MUSICKCL			
LOCUS	MUSICKCL	416 bp	15-MAR-1989
DEFINITION	Mouse IgG2ak rearranged kappa light-chain mRNA variable region		
ACCESSION	(V-J-kappa) anti-DNA autoantibody.		
NUM	M20828		
KEYWORDS	V-region; autoantibody; immunoglobulin kappa-chain; immunoglobulin light chain; immunoglobulin-kappa.		
SOURCE	Mouse (strain MRL/Mp -1pr/1pr) spleen hybridoma cell line MRL-DNA4, cDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphae; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 416) Kofler, R., Strohal, R., Balderas, R.S., Johnson, M.E., Noonan, D.J., Duchosal, M.A., Dixon, F.J., and Theofilopoulos, A.N.		
TITLE	Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice		
JOURNAL	J. Clin. Invest. 82, 852-860 (1988)		
MEDLINE	88331394		
COMMENT	Draft entry and computer-readable sequence [1] kindly submitted by R. Kofler 28-JUL-1988.		
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61	GATGTTGATGATCAAGTCAACTCTCCGCGCTGCACCCCTGGAGAACAGCTCT	120	
81	GATGTTGATGATCAAGTCAACTCTCCGCGCTGCACCCCTGGAGAACAGCTCT	140	
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141	ATCTCTTCAGGCTTAGTCAAGTCTTCCAAAGTTATGGGACACCTATTGTCTGG	200	
181	TACCTGCAAGAGCCCTGGGCACTCTCCAAAGTCTTCCAAAGTTATGGGACAC	240	
201	TACCTGCAAGAGCCCTGGGCACTCTCCAAAGTCTTCCAAAGTTATGGGACAC	260	

Tue May 11 13:50:12 1999

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Page 10

Qy 24.1 TCCTGGGCGCCAGACAGGTTAGTGGGAGAGGCTCAGGAGCAAGTTTCAACATCAAGATC 300

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Qy 30.1 TCGCAGTAGAGGCGTGAAGAGCTGGAGTGTATTACTGCTTACAGGTACACATCATCAGCG 360

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Qy 36.1 TACAGTTTCGACAGGGGACCAAGGTGGAATAAATA 396

Db 38.1 TATAGTTTCGAGTCGGGAGCCAACTGGAAATAAATA 416

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 11, 1999, 11:44:16 ; Search time 479.58 Seconds
(without alignments)
1313.650 Million cell updates/sec

Title: US-08-700-737-20

Perfect score: 413
Sequence: 1 ATGAGTTCCTGTAGGCT.....AAACGGCTGATCGCGCCG 413

Scoring table: IDENTITY_NUC

Searched: 2002476 seqs, 762712212 residues

Database :

EST.*
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2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: gp_est1:*
11: gp_est2:*
12: gp_est3:*
13: gp_est4:*
14: gp_est5:*
15: gp_est6:*
16: gp_est7:*
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20: gp_est11:*
21: gp_est12:*
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25: gp_est16:*
26: gp_est17:*
27: gp_est18:*
28: gp_est19:*
29: gp_est20:*
30: gp_est21:*
31: gp_est22:*
32: em_est10:*
33: em_est11:*
34: em_est12:*
35: em_est13:*
36: em_est14:*
37: em_est15:*
38: em_est16:*
39: em_est17:*
40: em_est18:*
41: em_est19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	243.4	58.9	442	24	AA405415	z56d02.r
2	237.2	57.4	488	11	H25625	H25625 y148g05.r1

3	227.4	55.1	363	20	AA464313	AA464313 zx78c12.r
4	215.4	52.2	467	11	H27034	H27034 y165d05.r1
5	200.4	48.5	374	24	AA602059	AA602059 nc05b02.s
6	192.6	46.6	357	11	T29104	T29104 EST69270 Ho
7	191.8	46.4	359	11	T27587	T27587 EST100475 H
8	183.4	44.4	430	12	H69156	H69156 y786f06.r1
9	182.8	44.3	335	24	AA402204	AA402204 z44f03.r
10	179.4	43.4	287	21	AA496610	AA496610 zv38g06.r
11	177.2	42.9	445	10	R48141	R48141 y166c09.r1
12	160.4	38.8	470	12	H62115	H62115 y440p01.r1
13	159	38.5	400	20	AA456778	AA456778 zw27f11.r
14	155.4	37.6	257	17	R51193	R51193 y771a07.r1
15	155.4	37.6	246	27	AA871804	AA871804 vq41c03.r
16	150.8	36.5	398	10	AA423447	AA423447 ve08a03.r
17	149.8	36.3	248	24	AA430449	AA430449 zw20f11.r
18	146.2	35.4	420	30	AT120005	AT120005 uc25e04.r
19	144	34.9	240	24	AA418046	AA418046 zv33c09.r
20	137.6	33.3	370	17	AA295093	AA295093 EST100400
21	137.2	33.2	353	10	T72954	T72954 y65a09.r1
22	134.8	32.6	418	21	AA515239	AA515239 ng69c07.s
23	134	32.4	253	17	AA295941	AA295941 EST101165
24	132.6	32.1	403	18	AA345486	AA345486 EST51505
25	131	31.7	349	18	AA379044	AA379044 EST91999
26	130.8	31.7	383	11	T29916	T29916 EST99871 Ho
27	130.6	31.6	364	11	T27579	T27579 EST100049 H
28	130.2	31.5	393	11	T27593	T27593 EST100653 H
29	129.4	31.3	413	17	AA301347	AA301347 EST14279
30	128.8	31.2	328	17	AA295311	AA295311 EST100471
31	127	30.8	405	18	AA360223	AA360223 EST69341
32	126.6	30.7	339	25	AA710249	AA710249 vt49e01.r
33	126.2	30.6	326	10	T73028	T73028 y65a09.r1
34	125.2	30.3	203	11	H39743	H39743 y653d07.r1
35	123.6	29.9	338	17	AA321464	AA321464 EST32940
36	121.8	29.5	300	17	AA300994	AA300994 EST13943
37	120	29.1	363	17	AA300651	AA300651 EST13764
38	119	28.8	405	10	R48845	R48845 y165f10.r1
39	118.6	28.7	262	18	AA377807	AA377807 EST90452
40	118.2	28.6	346	17	AA300582	AA300582 EST13427
41	118.2	28.6	242	21	AA479857	AA479857 z35b05.r
42	118	28.5	366	11	H27048	H27048 y165f06.r1
43	117.8	28.5	463	11	R69532	R69532 y782d09.r1
44	117.4	28.4	383	11	T27870	T27870 EST19007 Ho
45	115.8	28.0	294	18	AA366461	AA366461 EST77408

ALIGNMENTS

RESULT 1
AA405415 442 bp mRNA EST 09-NOV-1997
LOCUS z56d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741987
DEFINITION 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION
(HUMAN); mRNA sequence.
ACCESSION AA405415
NID 92063652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-MCI human EST Project
TITLE Unpublished (1997)
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

	RESULT	3			
	A4664313				
	LOCUS				
	DEFINITION	AA4664313	363 bp	mRNA	EST
		xz78c2.c1 Soates ovary tumor NBH0T Homo sapiens cDNA clone 80987B			10-JUN-1997
		5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION			
	(HUMAN) ; mRNA sequence.				
	ACCESSION	AA4664313			
	NID	G2I89197			
	KEYWORDS	EST.			
	SOURCE	human.			
	ORGANISM	Homo sapiens			
		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;			
		Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;			
		Homo.			
	REFERENCE	1 (bases 1 to 363)			
	AUTHORS	Killier,L., Allen,M., Bowles,I., Dubuque,T., Geisel,G., Jost,S., Kicaba,T., Lacy'M., Le,N., Lennon,G., Marra,M., Martin,D., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Wille,Y., Wylie,T., Waterston,R. and Wilson,R. Wash-Merck Est Project 1997 Unpublished (1997)			
	TITLE	JOURNAL			
	COMMENT				

FEATURES
 Contact: Wilson RK
 Mashu-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LINTL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28ml3 rev2 ET from Amersham.
 Location/Qualifiers

FEATURES	SOURCE
Location/Qualifiers	1 .363
/organism="Homo sapiens"	
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTACCACTGATCGAGTGGAGCGCCGCGGTTTTTTTTTTTTTTT 3'), double-stranded cDNA was site selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."	
/db_xref="taxon:9606"	
/clone="809878"	
/clone_lib="Soares ovary tumor NbHOT"	
/sex="Female"	
/tissue_type="ovarian tumor"	
/lab_host="DH10B (ampicillin resistant)"	
<1 .>363	
/db_xref="GDB:6039712"	
81 a 94 c 95 g 93 t	

Query Match	55.1%	Score 227.4	DB 20	Length 363
Best Local Similarity	77.3%	Pred. No. 3.6e-61		
Matches 276	Conservative 0	Mismatches 81	Indels 0	Gaps 0
QY	47	CTGTTCGGAGATGATGTTGATGATGACCTCAAGTCACCTCTCCCTGCTGCACCCCTG	106	
Db	5	CTGATCCAGTGGGGATATTGTGATGACCTCAAGTCACCTCTCCCTGCTGCACCCCTG	64	
QY	107	GAGAACCAAGCTTCATATCTCTTGCAAGGCTCTAGTAGAGTCTTGCAAGAGATTGGAACA	166	
Db	65	GAGAGCCGGCCCTCATCTCTCTGCAAGGCTCTAGTAGAGTCTCTGCAATATATGATCA	124	
QY	167	CCATATTGCTCTTGATCTGCACAGAGCCTGGCAGATCTCACAGCTCCATCTATGGA	226	
Db	125	ACATATTGGATGGTACTCTGCAGAGCGAGGAGCTCTCACAGCTCCATCTATTTGG	184	
QY	227	TTTCCAAACAGATTTTCTGGGGTGCCACAGAGTTCAAGTGGACATGGGACAGATT	286	

Db 185 GTTCAATCGGGCCCTCCGGGCTCCCTGACAGTTCAAGTGGAGTGCAGGACACAAATT 244

QY 287 TCACACTAAAGATCTCCGGAATAGAGCTGAGACGTGGAGTGTATTACTGCTTACAAAG 346

Db 245 TTACACTAAAATATCAGCAGATGTGAGGCTGAGGATGTGTGGGCTTATTACTGCAATGCAG 304

QY 347 GTACACATCAGACCGTACACGTTTGGACAGGGGACCAAGGTGAATTAACCGGCGCTG 403

Db 305 CTCATCAAACTTATTCATCTTTCGGCCCTGGGACCAAGTGGATATCAACAGAACTG 361

RESULT	4			
H27034				
LOCUS				
DEFINITION				
ACCESSION				
NID				
KEYWORDS				
SOURCE				
	H27034	467 bp	mRNA	EST 12-JUL-1995
	Y165d05.r1 Homo sapiens CDNA clone 163113 5'			similar to gb:X72466
	IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN)..			
	H27034			
	987024			
	Human clone=163113 library=Scars breast 3NbHst vector=pt773D			

SOURCE	ORGANISM
human clone-163313 library-Soares breast 3NbHst vector-pT773d (Pharmacia) with a modified polylinker box-Dh10b (ampicillin resistant) primer-M13Pr1 RSite1-not I RSite2-Eco RI Adulter human, 1st strand cDNA was primed with a Not I - 0149(04P) primer [5', TGTACCACATCTCAAGTGGAGGCGGCCCTTTTCTTTTCTTTTCTTTT 3']	Homo sapiens
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo.	Homo sapiens

REFERENCE
AUTHORS
 Chomsky, L.
 Homo sapiens
 Homo sapiens
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomia; Osteichthyes
 Saccropterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 467)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The Washu-Merc EST Project
 unpublished (1995)

```

FEATURES
  source
    Contact: Wilson RK
    WashU-Merck EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    High quality sequence stops: 352
    Source: IMAGE Consortium, LNL
    This clone is available royalty-free through LNL ; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    Location/Qualifiers
      1..467
        /organism="Homo sapiens"
        /clone="163113"
BASE COUNT
  96 a      122 c      122 g      123 t      4 others
ORIGIN

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Best Local Similarity	76.5%	Pred. No. 2.2e-57		
Matches 264	Conservative 0	Matches 81	Indels 0	Gaps 0
QY	1	ATGAAGTTCCTGTAGACGTGGTGGTGTCTGTGTCTGGATTCCTGTTCCGGAAGT	60	
Db	3	ATGAGCGTCCCTGTCACACTCCTGGGCTGTATGCTCTGGGCTCTGGATTCAGATGGG	62	
QY	61	GATGTTGATGACTCAAAAGTCACACTCCCTGGCTGTACACCCCTGGAAACAGACTTCT	120	

Db 63 GATATTGATGACTCACTCTCCACCTCCAGCCCTGAGAGCCGCCCTCC 122
 QY 121 ATCTTGGAGAGTCTAGTCAGAGTCTTGCAGAGATTATGGAGACCACTATTGCTTGG 180
 Db 123 ATCTCTGCAAGCTTAGTCAGAGCTCTTACATAGTATGATGATGATTTGGATTGG 182
 QY 181 TACCTGCAGAGAGCTGGCAGCTCTCCACAGCTCTCATCTTATGGATTTCACAGATT 240
 Db 183 TACCTGCAGAGAGCTGGCAGCTCTCCACAGCTCTCATCTTATGGATTTCAGAGGCGC 242
 QY 241 TCTGGGGTCCAGACAGTTCAGTGGCAGTGTTCAGGAGACAGATTTCACACTCAATC 300
 Db 243 TCCGGGCTCCAGAGCTTACAGTGGCAGTGTTCAGGAGACAGATTTCACACTCAATC 302
 QY 301 TCCGAGTAGAGCTGAGAGCTGGAGTGTATTACTGCTTACCA 345
 Db 303 AGTAGAGTAGAGCTGAGAGTGTGCTTTATTACTGATGCA 347

RESULT 5
 AA602059 374 bp mRNA EST 08-OCT-1997
 LOCUS n095b02.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1114539
 DEFINITION similar to gb:X55400.cosl IG KAPPA CHAIN PRECURSOR V-II REGION
 (HUMAN); contains Alu repetitive element; mRNA sequence.
 AA602059
 NID 92435848
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 374)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai,
 M.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: David B. Kitzman, Ph.D.
 DNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMW at:
 www-bio.liml.gov/bdip/image/image.html

FEATURES
 SOURCE
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 Seq primer: -40ml3 fwd, fr from Amersham
 High quality sequence stop: 369.
 Location/Qualifiers
 1. 374

/organism="Homo sapiens"
 /note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from
 5,000-10,000 microdissected preneoplastic cells
 histologically-determined to be prostatic intraepithelial
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the
 cDNA with an adaptor-specific primer, and the resulting
 PCR product subcloned into pAMP10 by the DBC-cloning
 method (Life Technologies). Average insert size is 600
 bp. NOTE: Not directionally cloned. This library was
 constructed by David Kitzman."
 /db_xref="taxon:9606"
 /clone="IMAGE:1114539"
 /clone_lib="NCI_CGAP_P22"
 /sex="Male"
 /dev_stage="45 years old"

BASE COUNT 78 a 105 c 102 g 89 t
 ORIGIN

Query Match 48.5%; Score 200.4; DB 24; Length 374;
 Best Local Similarity 73.7%; Pred. No. 1e-52;
 Matches 255; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 ATGAGTTGCTGTAGGCTGTGGCTCTCTCTGTTGTTGATTCCTGTTCCGGAGT 60
 Db 29 ATGAGGCTCTTGTCTCAGCTTCTGGGCTGTATGCTGTGGGCTCTGATGAGTGG 88
 QY 61 GATGTTGATGATCAAGATCAGCTCTCCCTGCTTCAACCCCTGAGAGACAGCTTCT 120
 Db 89 GATATGTGATGAGACCAAGACTCAGCTCTCCACCTTCAACCCCTGAGAGCGGCTCC 148
 QY 121 ATCTCTGCAAGCTTACAGAGTCTTGCAGAAAGATTATGGAAACACCTATTGCTTGG 180
 Db 149 ATCTCTGCAAGCTTACAGAGTCTTGCAGAAAGATTATGGAAAGACCTATTGAGCTGG 208
 QY 181 TACCTGCAGAGAGCTGGCCAGCTCTCCACAGCTCTCTATGATGGATTCCACAGATT 240
 Db 209 CTGACACAGAGCCAGCCAGCTCTCCAGACTCTTATATAGACTTCAACGGGTTT 268
 QY 241 TCTGGGGTCCAGACAGAGTTCAGTGGCAGTGTTCAGGAGACAGATTTCACACTCAATC 300
 Db 269 TCTGGGGTCCAGACAGAGTTCAGTGGCAGTGTTCAGGAGACAGATTTCACACTCAATC 328
 QY 301 TCCGAGTAGAGCTGAGAGCTGGAGTGTATTACTGCTTACAG 346
 Db 329 AGTAGAGTAGAGCTGAGAGTGTGCTTTATTACTGATGCA 374

RESULT 6
 T29104 357 bp mRNA EST 06-SEP-1995
 LOCUS EST692720 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
 DEFINITION light chain V region (GB:X54248) (HT:3095).
 T29104
 ACCESSION 9611202
 NID
 KEYWORDS EST.

SOURCE human primer-M13 Reverse library=Human Lymphoid tissue.

ORGANISM Homo sapiens
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 357)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bull,C.J., Lee,N., Kitzman,D.P., Cantor,M., Lander,E.S., White,C.J.,
 Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W.,
 Clayton,R.A., Cline,R.T., Cotton,M.D., Eale,Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.S.,
 Kelley,J.M., Klimke,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
 Merrick,J.M., Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T.,
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
 Sander,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterbeck,T.R.,
 Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
 Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
 Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,W.R., Rosen,C.A.,
 Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 52 Million Basepairs of cDNA Sequence
 Unpublished (1995)

JOURNAL Other_ESTS: EST69269
 COMMENT Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Galtherburg, MD 20878

Fischer, C., Hastings, G. A., He, W.-W., Hu, J.-S., Greene, J. M., Gruber, J., Hudson, P., Kim, A., Kozak, D. L., Kunsch, C., Ji, H., L. Weissner, P. S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;


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Db      126  AGGCACATGATTTTACACATCGAATAAATACAGAGGGGTGAGGCTGAGGATGTGTGGAGTTTATA 185
Oy      336  CTGCTTACAGAGTACACATCAGCCGTACACGTTGGACAGGGGACCAGATGGGAATTA 395
Db      186  CTGCATGCAAGATATAGAGTTTCTTGTGACCTTTGGCCAGGAGGACCAAGCTGAGATCAA 245
Oy      396  ACGGGCTGATG 406
Db      246  ACGAACTGTG 256

RESULT 13
AA456778
LOCUS      AA456778      400 bp      mRNA      EST      06-JUN-1997
DEFINITION zw27f11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770541
5' similar to gp:X06764 IG KAPPA CHAIN PRECURSOR V-III REGION
(HUMAN); mRNA sequence.
ACCESSION AA456778
NID      g2177199
KEYWORDS EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Homnidae;
REFERENCE      1 (bases 1 to 400)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE      Washu-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT
Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..400
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pRT73D (Pharmacia) with a
modified polylinker; Site_1: Not I - Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTCACATCTGAGTGGAGCGCGCCGCGGTTTTTTTTTTTTTTT 3') ,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaudo."
/db_xref="taxon:9606"
/clone="770541"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
<1..>400
/db_xref="GDB:5980414"
BASE COUNT      90 a 120 c 106 g 84 t
ORIGIN
Query Match      38.5%; Score 159; DB 20; Length 400;
Best Local Similarity      67.1%; Pred. No.9.5e-40;
Matches      261; Conservative      0; Mismatches      115; Indels      13; Gaps      2

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RESULT	14
R51193	
LOCUS	R51193
DEFINITION	R51193 257 bp mRNA EST 18-MAY-1995
DESCRIPTION	yj71a07.r1 Homo sapiens cDNA clone 154164 5' similar to gb:U72467
ACCESSION	IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN)..

ORGANISM	REFERENCE	AUTHORS
Homo sapiens		
Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata: Deuterostomia: Chordata: Vertebrata: Gnathostomata: Osteichthyes: Sarcopterygii: Chosnata: Tetrapoda: Amniota: Mammalia: Theria: Eutheria: Archonta: Primates: Catarrhini: Hominiidae: Homo: 1 (bases 1 to 257)		
Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,		

TITLE
JOURNAL
COMMENT
The Washu-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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Email: estewartson.w@stl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LINT; contact the

Query Match	37.68;	Score 155.4;	DB 10;	Length 257;
Best Local Similarity	73.58;	Pred. No. 1.1e-38;		
Matches 189; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0

RESULT	15
AA871804	
LOCUS	AA871804 246 bp mRNA
DEFINITION	vc41c03.r1 Barstead bowel MPLRB9 Mus musculus cDNA clone 109680
	EST 16-MAR-1998

ACCESSION	similar to gb:XI2431 IG KAPPA CHAIN V-II REGION (HUMAN);, mRNA sequence.
NID	AA871804
KEYWORDS	g2967249
SOURCE	EST.
ORGANISM	house mouse.
REFERENCE	Mus musculus.
AUTHORS	Mus musculus. Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus. 1 (bases 1 to 246) Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, T., Morris, M., Schellenger, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The WashU-HHWI Mouse EST Project Unpublished (1996)
TITLE	
JOURNAL	
COMMENT	

CONTACT: Marra M/Mouse EST Project
 WashU-HM1 Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
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 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMaG Consortium (info@image.llnl.gov) for further information.
 MGI:603036
 Seq primer: -28m13 rev2 ET from Amersham.
FEATURES
 source
 Location/Qualifiers
 1..246
 /organism="Mus musculus"
 /strain="FVB/N"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker: Site.1: EcoRI; Site.2: NotI; 1st strand cDNA
 was primed with a Not I - oligo(dn) primer [5'
 TGTTCAGATCTGAGTGGAGGCGCGCCCTTTTCTTTTCTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 [AATTCGATCCTTG], digested with Not I and cloned into the
 Not I and Eco RI sites of the modified pT73 vector.
 Source irradiated bowel harvested 72 hours after
 irradiation (1400 Gys). Library constructed by Bob
 Barstead "

/db_xref="taxon:10090"
 /clone="1096804"
 /clone_lib="Barstead bowel MPLRB9"
 /tissue_type="bowel"
 /dev_stage="8 weeks"
 /lab_host="DH10B"

BASE COUNT 59 a 66 c 51 g 70 t
 ORIGIN

Query Match 37.6%; Score 155.4; DB 27; Length 246;
 Best Local Similarity 82.7%; Pred. No. 1.1e-38;
 Matches 191; Conservative 0; Mismatches 36; Indels 4; Gaps 1;

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QY 1 ATGAGTTCCTGTAGGCTGTGCTCTGTGTTGATTCCTGTTCCGAGGT 60
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Db 20 ATGAGTTCCTGTAGGCTGTGCTCTGTGTTGATTCCTGTTCCGAGGT 75
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QY 61 GATGTGTGATGATCAAGTCCACTCCCGCTGTCAOCCCGAGAACCAAGCTCT 120
    |||||||
Db 76 GATGTGTGATGATCAAGTCCACTCCCGCTGTCAOCCCGAGAACCAAGCTCT 135
    |||||||

QY 121 ATCTCTGAGGTCTAGTCAGAGTCTTCAAGAGTATGAGAACCACTATTGCTTGG 180
    |||||||
Db 136 ATCTCTGAGGTCTAGTCAGAGTCTTCAAGAGTATGAGAACCACTATTGCTTGG 195
    |||||||

QY 181 TACCTGAGAAAGCTGTCCACAGCTCTCATCTATGAGATTTC 231
    |||||||
Db 196 TACCTGAGAAAGCTGTCCACAGCTCTCATCTATGAGATTTC 246
    |||||||

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Search completed: May 11, 1999, 11:44:17
 Job time: 504 sec

OM nucleic - nucleic search, using SW model

Run on: May 11, 1999, 12:03:35 ; Search time 88.51 Seconds
(without alignments)
877.846 Million cell updates/sec

Title: US-08-700-737-20

Sequence: 1 ATGAGTGCCTGTTAGCT.....AACGGCTGATGCGGCC 413

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	411.4	99.6	413	1	V20075	DNA encoding the 1
2	374.6	90.7	535	1	V20086	Consensus DNA sequ
3	360.8	87.4	396	1	V20077	DNA encoding murin
4	299.4	72.5	717	1	T62934	Murine anti-porcine
5	299.4	72.5	5300	1	T62938	3F4 human IgG4 exp
6	297.8	72.1	537	1	Q14651	Re-5-D6 anti-ICAM
7	294.6	71.3	394	1	Q62803	Humanised murine R
8	294.6	71.3	394	1	T88870	Humanised anti-KC-
9	294.6	71.3	717	1	T88870	L chain subunit of
10	294.6	71.3	717	1	V66756	Anti-human Fas mon
11	293	70.9	537	1	Q14801	Encodes murine ant
12	293	70.9	447	1	T31332	Anti-Idiotypic mon
13	291.4	70.6	394	1	Q62790	Humanised murine E
14	286.6	69.4	394	1	Q62788	Murine KC-4 immuno
15	286.6	69.4	394	1	Q62788	Murine KC-4 immuno
16	286.6	69.4	420	1	V60831	Variable light chain
17	286	69.2	427	1	Q36539	Chimeric MAb light
18	286	69.2	427	1	Q36536	BR5-2 light chain
19	285	69.0	394	1	Q87531	VL sequence of anti
20	284.4	68.9	424	1	T98835	Coding sequence of
21	283.8	68.7	396	1	V37265	CDNA encoding a va
22	283.4	68.6	394	1	Q62779	CDNA encoding a va
23	283.4	68.6	394	1	Q62774	Murine BrE-3 immu
24	282.8	68.5	8897	1	V18662	Murine BrE-3 immu
25	282.4	68.4	434	1	Q36534	Plasmid pTWD-CpV
26	281.2	68.1	384	1	V56383	BR5-2 murine IgG3
27	281.2	68.1	384	1	V54857	Murine ICR-8.1 V-K
28	280	67.8	489	1	Q11292	Murine antibody IC
29	278.6	67.5	388	1	V66674	Encodes murine mon
30	273.2	66.2	422	1	V22075	Anti-Fas MAb CH11
31	272.8	66.1	432	1	Q08606	DNA encoding the 1
32	272.8	66.1	861	1	T81500	Co-1 Light Chain V
33	272.8	66.1	432	1	T43459	sFV anti-rev sequen
34	272.8	66.1	861	1	T45337	MAb Co-1 light cha
35	269	65.1	720	1	V61359	Single chain sFV a
36	267.4	64.7	720	1	V61360	Anti-human Fas hum
37	267.4	64.7	720	1	V61361	Anti-human Fas hum
38	266.8	64.6	8897	1	V18633	Plasmid pDI6hJ1.LI
39	266	64.4	375	1	V56402	Human ICR-8.1 V-K
40	265.8	64.4	375	1	V54860	Humanised murine a
41	265.8	64.4	720	1	V61362	Anti-human Fas hum
42	261.2	63.2	330	1	Q43746	Sequence encoding
43	257	62.2	782	1	Q86755	Anti-dansyl single

ALIGNMENTS

RESULT 1
 ID V20075 standard; DNA: 413 BP.
 AC V20075.
 AT 14-JUL-1998 (first entry)
 DE DNA encoding the light chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MacCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 PH Key
 FT CDS Location/Qualifiers
 FT 1..413 /tag= a
 FT /transl_except= (pos: 412..413, aa: Pro)
 FT /note= "no stop codon given"
 FT sig_peptide 1..60 /tag= b
 FT mat_peptide 61..413 /tag= c
 FT WO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 DR WPI; 98-159172/14.
 DR P-PSDB; W53812.
 PR Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PR used for treating inflammatory disease, pancreatitis, diabetes,
 PR asthma, graft versus host disease and sarcoidosis
 PS Claim 17; Fig 12, 145pp; English.
 CC The present sequence encodes the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MacCAM-1, which is present of high endothelial
 CC venules in muscosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 413 BP; 90 A; 96 C; 116 G; 111 T;

QY 181 TACCTGCAGAAAGCTGCGCCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATTT 240
 DB 181 TACCTGCAGAAAGCTGCGCCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATTT 240
 QY 241 TCTGGGGTCCAGACAGGTTGAGTGCAGTGTTCAGGAGACAGATTTCACACTCAAGTTC 300
 DB 241 TCTGGGGTCCAGACAGGTTGAGTGCAGTGTTCAGGAGACAGATTTCACACTCAAGTTC 300
 QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATTACTGCTTACAGATTCACATCAGCCG 360
 DB 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATTACTGCTTACAGATTCACATCAGCCG 360
 QY 361 TACACGTTCCGACAGGAGGACCAAGTGTAAATAAACGGGCTGATGCGCGCC 413
 DB 361 TACACGTTCCGACAGGAGGACCAAGTGTAAATAAACGGGCTGATGCGCGCC 413

RESULT 2
 V20086 standard; DNA; 535 BP.
 ID V20086;
 AC V20086;
 DT 14-JUL-1998 (first entry)
 DE Consensus DNA sequence of the murine variable light chain region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised adressin cell adhesion molecule-1; MadCAM-1;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.
 FH Key
 FT CDS Location/Qualifiers
 FT 16..435
 FT /tag- a
 FT /note= "no stop codon given"
 FT sig_peptide
 FT 16..75
 FT /tag- b
 FT mat_peptide
 FT 76..435
 FT /tag- c

MO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J;
 DR WPI: 98-159172/14.
 DR P-PSDB: W53817.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3; 145pp; English.
 CC The present sequence represents the consensus nucleotide sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC addressin molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 535 BP; 126 A; 128 C; 132 G; 149 T;

Matches 389; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 ATGAAGTTGCTGCTTAGAGCTTTGCTCTTCTGTTCTTGAGATTCTGTTCCGAGGT 60
 DB 16 ATGAAGTTGCTGCTTAGAGCTTTGCTCTTCTGTTCTTGAGATTCTGTTCCGAGGT 75
 QY 61 GATGTTGTGATGACTCAAGTCCACTCTCTCCCTGCTTACCCCTGAGAACAGCTTCT 120
 DB 76 GATGTTGTGATGACTCAAGTCCACTCTCTCCCTGCTTACCCCTGAGAACAGCTTCT 135
 QY 121 ATCTCTTGACAGCTTAGTCAGAGTCTTGCAAGAGTATGGAGACACTATTGCTTGG 180
 DB 136 ATCTCTTGACAGCTTAGTCAGAGTCTTGCAAGAGTATGGAGACACTATTGCTTGG 195
 QY 181 TACCTGCAGAAAGCTGCGCCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATTT 240
 DB 196 TACCTGCAGAAAGCTGCGCCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATTT 255
 QY 241 TCTGGGGTCCAGACAGGTTGAGTGCAGTGTTCAGGAGACAGATTTCACACTCAAGTTC 300
 DB 256 TCTGGGGTCCAGACAGGTTGAGTGCAGTGTTCAGGAGACAGATTTCACACTCAAGTTC 315
 QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTGTATTACTGCTTACAGATTCACATCAGCCG 360
 DB 316 AGCACATAAAGCTTGAGAGTGTGATGCTTACAGGTTACACATCAGCCG 375
 QY 361 TACACGTTCCGACAGGAGGACCAAGTGTAAATAAACGGGCTGATGCGCGCC 413
 DB 376 TACACGTTCCGACAGGAGGACCAAGTGTAAATAAACGGGCTGATGCTGCGCC 428

RESULT 3
 V20077 standard; DNA; 396 BP.
 ID V20077;
 AC V20077;
 DT 14-JUL-1998 (first entry)
 DE DNA encoding murine Act-1 light chain variable region.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised adressin cell adhesion molecule-1; MadCAM-1;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease; ss.
 OS Mus sp.
 FH Key
 FT CDS Location/Qualifiers
 FT 1..396
 FT /tag- a
 FT sig_peptide
 FT 1..60
 FT /tag- b
 FT mat_peptide
 FT 61..396
 FT /tag- c

MO9806248-A2.
 PD 19-FEB-1998.
 PF 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J;
 DR WPI: 98-159172/14.
 DR P-PSDB: W53814.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 26; Fig 7; 145pp; English.
 CC The present sequence encodes the light chain variable region of
 CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
 CC integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a
 CC ligand of this particular integrin. The Act-1 antibody interferes with
 CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
 CC endothelial venules in muscosal lymph nodes. Humanised Act-1 can be used
 CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
 CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can

Query Match: 90.7%; Score 374.6; DB 1; Length 535;
 Best local Similarity 94.2%; Pred. No. 4.1e-115;

CC also be used for detection, isolation and diagnosis.
 CC Sequence 396 BP; 92 A; 89 C; 102 G; 113 T;

Query Match 87.4% Score 360.8; DB 1; Length 396;
 Best Local Similarity 94.4%; Pred. No. 1.4e-110;
 Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGAAGTTGCTGTAGGCTGTGGTCTGTGTTCTGGATTCCTGTTCCGAGGT 60
 DB 1 ATGAAGTTGCTGTAGGCTGTGGTCTGTGTTCTGGATTCCTGTTCCGAGGT 60
 QY 61 GATTTGTGATGACTCAAAATCCACTCTCCCTGCTGACCCCTGAGAACAGCTTCT 120
 DB 61 GATTTGTGATGACTCAAAATCCACTCTCCCTGCTGACCCCTGAGAACAGCTTCT 120
 QY 121 ATCTCTTGACAGTCTAGTCAAGTCTTGCAGAGTTATGGAGACACTATTGCTTGG 180
 DB 121 ATCTCTTGACAGTCTAGTCAAGTCTTGCAGAGTTATGGAGACACTATTGCTTGG 180
 QY 181 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCTCATCTATGAGATTCCACAGATT 240
 DB 181 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCTCATCTATGAGATTCCACAGATT 240
 QY 241 TCTGGGGTGCAGACAGGTTGACAGTGCAGTTCAGGAGACAGATTTCACACTCAAGATC 300
 DB 241 TCTGGGGTGCAGACAGGTTGACAGTGCAGTTCAGGAGACAGATTTCACACTCAAGATC 300
 QY 301 TCGGAGTAGAGGCTGAGAGCTGTATTTACTCTTACAGAGTTCACATCAGCCG 360
 DB 301 TCGGAGTAGAGGCTGAGAGCTGTATTTACTCTTACAGAGTTCACATCAGCCG 360
 QY 361 TACAGCTTCGGACAGGGGACCAAGTGAATAA 396
 DB 361 TACAGCTTCGGACAGGGGACCAAGTGAATAA 396

RESULT 4

T62934
 ID T62934 standard; DNA; 717 BP.

DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 3F4 light chain DNA sequence.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Mus sp.
 PN W03711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans WJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR P-PSDB: W14937.
 DR WPI: 97-212855/19.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure; Page 52-53; 105pp; English.
 CC DNA sequences (T62934-35) respectively code for the light chain
 CC (W14937) and heavy chain (W14938) of murine anti-porcine soluble
 CC vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb)
 CC 3F4. Hybridoma 3F4 was produced by standard techniques using
 CC recombinant, soluble porcine VCAM as immunogen. Chimeric
 CC antibodies can be produced by cloning MAb 3F4 and 2A2 (see also
 CC T62929-30) variable regions into expression plasmid PAPEX-3P
 CC modified to contain the human gamma4 constant region in place of
 CC the human gamma1 C1 region. Sequences are provided for 3F4
 CC (chimeric) human G2/G4 cDNA (T62936), a 3F4 human G2/G4 expression
 CC plasmid insert (T62937), and a 3F4 human IgG4 expression plasmid
 CC insert (T62938). The chimeric antibodies are specific for porcine

CC VCAM. They are useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine
 CC cells, tissues and organs into human recipients.
 CC Sequence 717 BP; 185 A; 184 C; 182 G; 166 T;

Query Match 72.5% Score 299.4; DB 1; Length 717;
 Best Local Similarity 84.5%; Pred. No. 4.4e-90;
 Matches 349; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGAAGTTGCTGTAGGCTGTGGTCTGTGTTCTGGATTCCTGTTCCGAGGT 60
 DB 1 ATGAAGTTGCTGTAGGCTGTGGTCTGTGTTCTGGATTCCTGTTCCGAGGT 57
 QY 61 GATTTGTGATGACTCAAAATCCACTCTCCCTGCTGACCCCTGAGAACAGCTTCT 120
 DB 58 GATTTGTGATGACTCAAAATCCACTCTCCCTGCTGACCTTGGAGATCAAGCTCC 117
 QY 121 ATCTCTTGACAGTCTAGTCAAGTCTTGCAGAGTTATGGAGACACTATTGCTTGG 180
 DB 118 ATCTCTTGACAGTCTAGTCAAGTCTTGCAGAGTTATGGAGACACTATTGCTTGG 177
 QY 181 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATT 240
 DB 178 TACCTGCAGAGCTGCGCAGTCTCCACAGCTCCTCATCTATGAGATTTCACAGATT 237
 QY 241 TCTGGGGTGCAGACAGGTTGACAGTGCAGTTCAGGAGACAGATTTCACACTCAAGATC 300
 DB 238 TCTGGGGTGCAGACAGGTTGACAGTGCAGTTCAGGAGACAGATTTCACACTCAAGATC 297
 QY 301 TCGGAGTAGAGGCTGAGAGCTGTATTTACTCTTACAGAGTTCACATCAGCCG 360
 DB 298 AGCAGAGTAGAGGCTGAGAGCTGTATTTACTCTTACAGAGTTCACATCAGCCG 357
 QY 361 TACAGCTTCGGACAGGGGACCAAGTGAATAA 413
 DB 358 TACAGCTTCGGACAGGGGACCAAGTGAATAA 410

RESULT 5

T62938
 ID T62938 standard; DNA; 5300 BP.

DT 16-JUN-1997 (first entry)
 DE 3F4 human IgG4 expression plasmid insert sequence.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis; ss.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 FH Key
 FT 903..1055 Location/Qualifiers
 FT /*tag- a
 FT 1056..1285
 FT /*tag- b
 FT 1286..2055
 FT /*tag- c
 FT /codon_start- 1350
 FT 2056..2445
 FT /*tag- d
 FT 2446..2481
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 FT 3026..3349
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 FT 4081..4233

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FT      Intron      /tag- k
FT      4234. 4463
FT      /tag- l
FT      4464. 5212
FT      /tag- m
FT      /codon_start- 4496
PN      MO9711971-A1.
PD      03-APR-1997.
PF      27-SEP-1996; U15575.
PR      28-SEP-1995; US-004489.
PR      26-SEP-1996; US-004489.
PA      (ALEX-) ALEXION PHARM INC.
PI      Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI      Rother RP;
DR      WPI: 97-212855/19.
DR      P-PSDB: W14941.
DR      P-PSDB: W14942.
PT      Antibodies binding to porcine but not human cell interaction
PT      proteins - useful to treat and assay for rejection of xenografted
PT      porcine organs, tissues or cells
PS      Disclosure: Page 61-67; 105pp; English.
CC      A DNA sequence (T62938) comprises a 3f4 human IgG4 expression
CC      plasmid insert sequence. It is obtd. by cloning the light chain
CC      (see also T62934) and heavy chain (see also T62935) variable
CC      region sequences of murine anti-porcine vascular cell adhesion
CC      molecule (VCAM) monoclonal antibody 3f4 into an expression plasmid
CC      modified to contain the human gamma4 constant region in plasmid of
CC      the human gamma C1 region. The encoded heavy chain (W14941) and
CC      light chain (W14942) can be used to produce a chimeric antibody
CC      that is specific for porcine VCAM. The chimeric antibody is useful
CC      for diagnosing human rejection of porcine xenotransplants and for
CC      improving xenotransplantation of porcine cells, tissues and organs.
CC      into human recipients.
SQ      Sequence 5300 BP; 1236 A; 1494 C; 1375 G; 1195 T;

Query Match      72.5%; Score 299.4; DB 1; Length 5300;
Best Local Similarity 84.3%; Pred. No. 1e-89;
Matches 349; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY      1 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTGTGTGAGTCTGCTGCGGAGT 60
DB      4496 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTGTGTGAGTCTGCTGCGGAGT 4552
QY      61 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAACCCCTGGAGAACAGCTTCT 120
DB      4553 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAAGTCTGGAGAACAGCTTCT 4612
QY      121 ATCTCTTGACAGGTCTAGTCAAGTCTGTGCAAGAGTTATGGGAACCTTATTTGCTTGG 180
DB      4613 ATCTCTTGACAGGTCTAGTCAAGTCTGTGCAAGAGTTATGGGAACCTTATTTGCTTGG 4672
QY      181 TACTGTGAGAGCTGTGGCGAGTCTCCACAGTCTCTCATCTATGAGGATTCCACAGATT 240
DB      4673 TACTGTGAGAGCTGTGGCGAGTCTCCACAGTCTCTCATCTATGAGGATTCCACAGATT 4732
QY      241 TCTGGGGTCCAGACAGGCTTCAAGTGTGCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 300
DB      4733 TCTGGGGTCCAGACAGGCTTCAAGTGTGCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 4792
QY      301 TCCGCAAGTAGAGCTGAGAGCTGTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 360
DB      4793 AGCAGAGTGTGAGCTGTGAGATCTGTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 4852
QY      361 TACACGTTGGAGACAGGGGACCAAGGTGGAATAAAGGGCTGATGTGGGGGCC 413
DB      4853 TTCACGTTCCGAGGGGACCAAGGTGGAATAAAGGGCTGATGTGGGGGCC 4905

RESULT      6
ID      Q14651
AC      Q14651; standard; cDNA; 537 BP.
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DT      14-FEB-1992 (first entry)
DE      R6-5-D6 anti-ICAM-1 light chain.
KW      Intercellular adhesion molecule-1; antibody; chimeric; ds.
OS      Mus musculus.
FH      Key signal_peptide 19..75
FT      Location/Qualifiers
FT      /tag- a
FT      19..537
FT      cds
FT      /tag- b
PN      MO9116928-A.
PD      14-NOV-1991.
PF      29-APR-1991; U02946.
PR      27-APR-1990; GB-009548.
PA      (CELL-) CELTECH LTD.
PA      (BOEH) BOEHRINGER INGELHEIM PHA.
PI      Adair JR, Robinson MK, Bright SM, Rothlein RA;
PI      WPI: 91-353534/48.
DR      P-PSDB: R15199.
PT      New humanised chimeric anti-ICAM-1 antibodies - useful in
PT      treating inflammation e.g. psoriasis and ulcerative colitis to
PT      suppress metastasis of haematopoietic tumour cell and in
PT      diagnosis.
PS      Claim 10; Fig 1; 85pp; English.
CC      The sequence comprises the 5' untranslated region, signal sequence,
CC      variable region and part of the constant region for the R6-5-D6
CC      murine Mab light chain. The hybridoma cell line R6-5-D6 producing
CC      the anti ICAM-1 Ab was provided by Boehringer Ingelheim
CC      Pharmaceuticals Inc. The cells were grown and mRNA isolated and
CC      used to prepare cDNA for a library in pSP64 vector DNA. The
CC      library was grown in E. coli HB101 and colonies screened using a
CC      probe complementary to a sequence in the mouse kappa constant
CC      region or with a 980 bp BamHI-EcoRI restriction fragment of a
CC      previously isolated mouse IgG2a constant region clone. Six
CC      positive clones were isolated and rescreened. Positive clones from
CC      the second round of screening were grown and the DNA inserts
CC      sequenced. The DNA was used to construct humanised Abs having
CC      chimeric variable regions, esp. with IgG human constant region
CC      domains. The Abs can be used to treat inflammation, to suppress
CC      metastasis of haematopoietic tumour cells and growth of ICAM-1
CC      expressing tumour cells, to treat viral infection, to suppress
CC      extravascular migration of virally infected leucocytes and to treat
CC      asthma.
CC      See also Q14652 and Q14830.
SQ      Sequence 537 BP; 135 A; 134 C; 128 G; 139 T;

Query Match      72.1%; Score 297.8; DB 1; Length 537;
Best Local Similarity 84.3%; Pred. No. 1.3e-88;
Matches 348; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY      1 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTGTGTGAGTCTGCTGCGGAGT 60
DB      19 ATGAAGTGGCTGTAGAGCTGTGGTCTGTGTGTGTGAGTCTGCTGCGGAGT 75
QY      61 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAACCCCTGGAGAACAGCTTCT 120
DB      61 GATGTGTGATGACTCAAGTCCACTCTCCCTGCTGTCAAGTCTGGAGAACAGCTTCT 135
QY      121 ATCTCTTGACAGGTCTAGTCAAGTCTGTGCAAGAGTTATGGGAACCTTATTTGCTTGG 180
DB      121 ATCTCTTGACAGGTCTAGTCAAGTCTGTGCAAGAGTTATGGGAACCTTATTTGCTTGG 195
QY      181 TACTGTGAGAGCTGTGGCGAGTCTCCACAGTCTCTCATCTATGAGGATTCCACAGATT 240
DB      181 TACTGTGAGAGCTGTGGCGAGTCTCCACAGTCTCTCATCTATGAGGATTCCACAGATT 255
QY      241 TCTGGGGTCCAGACAGGCTTCAAGTGTGCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 300
DB      241 TCTGGGGTCCAGACAGGCTTCAAGTGTGCAAGTGTTCAGGAGACAGATTTCACACTCAAGATC 315
QY      301 TCCGCAAGTAGAGCTGAGAGCTGTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 360
DB      301 TCCGCAAGTAGAGCTGAGAGCTGTGGAGTGTATTACTGTCTTACAGGTACATCAACCG 375
```

QY 361 TACACGTTCCGACAGGGGACCAAGGTGGAATTAACCGGGCTGATGGGGCC 413
||||| ||||||| ||||||| ||||||| ||||| |||
Db 376 CTCACGTTCCGAGGGGGGACCAAGCTGGAATTAACCGGGCTGATGGTGACC 428

RESULT	7
Q62803	

DT 25-Jan-1995 (first entry)
DE Humanised murine KC-4 immunoglobulin light chain V-region DNA.
KW Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human mammary fat globule; human breast carcinoma
KW murine anti-HMG monoclonal antibody KC-4; humanised analogue; ss.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.

PN WO9411509-A.
PD 26-MAY-1994.
PE 16-NOV-1993; U11445.
PR 16-NOV-1992; US-977696.
PR 30-SEP-1993; US-129930.
PR 08-OCT-1993; US-134346.
PA (CANC-) CANCER RES. FUND CONTRA COSTA,
PI Cetani, RL, DO Couto FJR, Fadlan EA, Peterson JA;
PI WPI: 94-183510/22.
DR
DR P-PSDS: R528422.
PT New analogue peptide(s) comprising antibody variable regions -
PT used to develop prods. for use in the detection, diagnosis,
PT therapy and prevention of neoplasms
PS Example 67; Page 90; 109pp; English.
PS This DNA sequence encodes a humanised murine anti-human carcinoma
CC antibody, light chain variable region. The humanised antibody is
CC useful for carcinoma therapy and diagnosis and for in vivo imaging
CC of neoplastic cells. It is also of use in inhibiting the growth of
CC a primary or metastasised neoplasm.
SQ Sequence 394 BP; 97 A; 94 C; 98 G; 105 T;

Query Match	71.3%	Score 294.6;	DB 1,	Length 394;
Best Local Similarity	85.6%;	Pred. No. 1.3e-88;		
Matches 340; Conservative	0;	Mismatches 54;	Indels 3;	Gaps 1;

QY	1	ATGAAGTGGCGCTGTAGAGCTGTGTGGTGGTGTGTTGTTCTGATGATCCGTGTTCCGGAGT	60
Db	1	ATGAAGTGGCGCTGTAGAGCTGTGTGGTGGTGTGTTGTTCTGATGATCCGTGTTCCGGAGT	57
QY	61	GATGTGTGATGACTCAAAGTCACACTCCCTCCGCTGTACCCCTGGAGAACCAGCTTCT	120
Db	58	GATGTGTGATGACCAACACCTCTCTCCCTCCGCTGTACATCCAGGAGACCGCTCC	117
QY	121	ATCTCTTCAGAGCTAGTCAGAGCTCTTCGAAAGGTTATGGGAACCCATTTGCTTGG	180
Db	118	ATCTCTTCAGATCTAGTCAGAGAGATTGTATCATAGTATGGAACACCTATTTGAAATGG	177
QY	181	TACCGCGAAGAGCGTGGCGAGCTCCACAGCTCCATCTATGGGATTTCCACAGATTT	240
Db	178	TACCTGCGAAGAACCAAGCGCACTGTCCACAGCTCCTGTGATCTCAAAAGTTTCCATCCGATTT	237
QY	241	TCTGGGTTGCCAGACAGGTTGATGGCAGTGGTTCAGGAGCAGATTTACACTCAATC	300
Db	238	TCTGGGTTCCAGACAGGTTGATGGCAGTGGATTCAGGAGCAGATTTACACTCAATC	297
QY	301	TCCGAGTAGAGGCTGAGAGAGCTGGAGTGTATTAAGCTTTACAAGGTACACATCAGCG	360
Db	301	TCCGAGTAGAGGCTGAGAGAGCTGGAGTGTATTAAGCTTTACAAGGTACACATCAGCG	360

Db 298 AGCAGAGGAGGCGCTGAGGAGATGTGGGAATTATTATTACGTCTTCAAGGTTCAACATGTTCCG 35

Q7₁ 361 TACACGTTCCGACAGGGGACCAAGGTGGAAATTAAC 397

Db 358 TACACGTTCCGAGGGGGGACCAACCTGGAAATTAAC 394

RESULT	8
Q87533	
ID	Q87533 standard; DNA; 394 BP.

DT	27-OCT-1995	(first entry)	
DE	Humanised anti-KC-4 antibody	VL FR-HZ.	
KW	Anti-KC-4 antibody; humanised antibody; cancer; ss.		
OS	Synthetic.		
PH	key	Location/Qualifiers	
FT	cd8	1..393	
FT	cd8	/*tag- a	
PN	M09510776-A.		
PD	20-APR-1995.		
PF	16-NOV-1993: U11444.		
PR	08-OCT-1993: US-134346.		
PA	(CANC-) CANCER RESEARCH FUND CONTRA COSTA.		
PI	Cetaniati RL, Docouto JR, Peterson JA;		
PR	WPI: 95-161912/21.		

Query Match	71.3%	Score 294.6	DB 1	Length 394
Best Local Similarity	85.6%	Pred. No. 1.3e-88		
Matches 340	Conservative 0	Mismatches 54	Indels 3	Gaps 1

Qy	61	GATGTGGATGAC	TCMAAGTCACACTCCCTGGCTGACACCCTGGAGAACAGGCTCT	12
Db	58	GATGTTTGAATGAC	CCAAACTCTCTCTCCCTGGCTGTCACCTCCAGGAGACCACGCTCC	117
Qy	121	ATCTCTTCAGGTC	TAGTCACAGTCTTTGCAAGATTAATGGAACACCTATTGTCTTGG	180
Db	118	ATCTCTTCAGATCT	TAGTCACAGATTTGATAGTAAATGGAACACCTATTGTGATGG	177
Qy	181	TACCTGCAGAA	CGCTGGCCAGTCTTCACAGCTCCTCATCTATGSGATTTCCACAGATTT	240
Db	178	TACCTGCAGAA	CCAGGCGCACTCTCCACAGCTCCTGATCTCAAGTTCATCTCGATTT	237
Qy	241	TCTGGGGGCCAG	ACAGTTAGTGGGAGTGGTTCAGGAGACAGTTTCACACTCAATTC	300
Db	238	TCTGGGGTCCAG	ACAGGTTTAGTGGGAGTGGATCAGGAGACAGATTTTCACACTCAATTC	297
Qy	301	TCGCGAGTAGAG	GCGCTGAGAGAGTGGGAGTGTATTACTGCTTACAGGTACACATCACGCG	360
Db	298	AGCAGAGTAGAG	GCGCTGAGAGATGTGGGAATTATTACGTCTTCAAGGTTCACATGTTCCG	357
Qy	361	TACACGTTTGG	ACAGGAGCCAAAGTGGAAATTAATAC	397

Db 298 AGCAGAGTGGAGGCTGAGGATCTGGAGTTATTCTGCTCTCAAGTACATGTTCT 357
QY 361 TACACGTTCCGACAGGAGGACCAAGTGAATAAAGCGGCTGATGGCGCC 413
Db 358 CCGGCGTTCGTTGGAGGACCAACCTGAATCAAGGCGGTGATGCTGCACC 410

RESULT 11

Q14801
ID Q14801 standard; DNA; 537 BP.

AC Q14801:
DE 13-FEB-1992 (first entry)
DE Encodes murine anti-ICAM monoclonal antibody light chain.
KW Interleukin adhesion molecule; variable region; V(L); mouse;
KW R6-5-D6 murine MAb; complementarity determining region; CDR; ds.
OS Mus musculus.

FT Key Location/Qualifiers
FT CDS 19..537
FT /tag- a
FT /product- anti-ICAM_light_chain

WO9116927-A.
PD 14-NOV-1991.
PF 28-APR-1991: U029442.
PR 27-APR-1990: GB-009549.
PA (CELL-) CELTECH LTD.
PA (BOE) BOEHRINGER INGELHEIM PHA.
PI Adair JR, Althwal DS, Rothlein RA.
DR WPI: 91-353533/48.
DR P-SDB: R15059.

PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
PT and prevent inflammation (e.g. psoriasis) tumours, viral
PS Infections and asthma and in diagnosis
PS Disclosure: Fig 1; 83pp; English.
CC The light chain sequence was isolated from a cDNA library prep. from
CC hybridoma cell line R6-5-D6 which secretes murine IgG2a/kappa
CC antibody. The library was screened using a probe sequence
CC complementary to a sequence in mouse kappa constant region. The
CC murine framework-encoding sequences (i.e. not encoding CDRs) will be
CC replaced by human framework sequences to produce recombinant (CDR-
CC grafted humanised) antibody molecules having specificity for ICAM-1.
SQ Sequence 537 BP; 135 A; 132 C; 129 G; 140 T;

Query Match 70.9%; Score 293; DB 1; Length 537;
Best Local Similarity 83.5%; Pred. No. 5.2e-88;
Matches 345; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 ATGAAGTTGCTTTAGGCTGTGCTGCTTCTGTTCTGGATTCTGTTCCGAGGT 60
Db 19 ATGAAGTTGCTTTAGGCTGTGCTGCTTCTGTTCTGGATTCTGTTCCGAGGT 75
QY 61 GATGTTGATGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 120
Db 76 GATGTTGATGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 135
QY 121 ATCTCTGCAAGTCTAGTCAAGTCTGTCGAAGATTAGGAACACCTATTGCTTGG 180
Db 136 ATCTCTGCAAGTCTAGTCAAGTCTGTCGAAGATTAGGAACACCTATTGCTTGG 195
QY 181 TACCTGCAAGAGCTGGCCAGTCTCCACAGTCTCTCATATGAGGATTCCACAGATT 240
Db 196 TACCTGCAAGAGTCAAGGAGGAGTCTCCAAAGCTCTGATCTCAAAAGTTCCAAAGATT 255
QY 241 TCTGGGGTCCAGACAGGTTCAAGGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAG 300
Db 256 TCTGGGGTCCAGACAGGTTCAAGGAGGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 315
QY 301 TCGGAGTAGAGGCTGAGAGGAGTGTATTACTGCTTACCAAGGTACACATCAGCG 360
Db 316 AGGAGAGTAGAGGAGGAGGAGTGTATTACTGCTTACCAAGGTACACATCAGTTCT 375
QY 361 TACAGTTTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 413

Db 376 CTCACGTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 428

RESULT 12

T31332
ID T31332 standard; cDNA; 447 BP.

AC T31332;
DE 26-FEB-1997 (first entry)
DE Anti-idiotype monoclonal antibody 1A7 variable light chain, cDNA.
KW Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7;
KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
KW vaccine; treatment; palliate; detection; diagnosis;
KW recombinant production; purification; probe; primer; assay;
KW amplification; gene therapy; ss.

FT Key Location/Qualifiers
FT mat.peptide 1..446
FT /tag- a

WO9622373-A2.
PD 25-JUL-1996.
PF 17-JAN-1996: U00882.
PR 17-JAN-1995: US-372676.
PR 16-JAN-1996: US-372676.
PA (KENT) UNIV KENTUCKY.
PI Chatterjee M, Chatterjee SK, Foon KA.
DR WPI: 96-354530/35.
DR P-SDB: W03199.

PT Monoclonal antibody 1A7 and related polynucleotide(s) and
PT polypeptide(s) - useful to treat or palliate a GD2-associated
PT disease, e.g. melanoma and glioma
PS Claim 10; Fig 1; 141pp; English.
CC The present sequence encodes the murine anti-idiotype monoclonal
CC antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against
CC the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique
CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
CC density by human neuroectodermal tumours, e.g. malignant melanoma,
CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
CC or palliate such diseases. They can also be used in a vaccine to treat
CC the risk of recurrence of a clinically detectable tumour, and detect an
CC anti-GD2 Ab bound to a tumour cell.
CC MAb 1A7 overcomes immune tolerance and induces an immune response
CC against GD2, which comprises anti-GD2 Ab (humoral response) and
CC GD2-specific cells (cellular response). It can be used to purify
CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
CC anti-GD2 activity.
CC The cDNA can be used in expression systems for 1A7 prodn., and in
CC the prepn. of probes and primers to respectively assay for 1A7
CC cDNA, and amplify desired polynucleotides for use in gene therapy.
SQ Sequence 447 BP; 106 A; 110 C; 108 G; 123 T;

Query Match 70.9%; Score 293; DB 1; Length 447;
Best Local Similarity 83.5%; Pred. No. 4.8e-88;
Matches 345; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

QY 1 ATGAAGTTGCTTTAGGCTGTGCTGCTTCTGTTCTGGATTCTGTTCCGAGGT 60
Db 1 ATGAAGTTGCTTTAGGCTGTGCTGCTTCTGTTCTGGATTCTGTTCCGAGGT 57
QY 61 GATGTTGATGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 120
Db 58 GATGTTGATGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 117
QY 121 ATCTCTGCAAGTCTAGTCAAGTCTGTCGAAGATTAGGAACACCTATTGCTTGG 180
Db 118 ATCTCTGCAAGTCTAGTCAAGTCTGTCGAAGATTAGGAACACCTATTGCTTGG 177
QY 181 TACCTGCAAGAGCTGGCCAGTCTCCACAGTCTCTCATATGAGGATTCCACAGATT 240


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Db 58 GATGTTTGATGATCAACCACTCTCTCCCTGCTGACGCTTGAGATCAAGCCTCC 117...
QY 121 ATCTCTGACAGGTCTAGTCAGAGTCTTCCAAAGATTTGGACACCTATTCTTGG 180
Db 118 ATCTCTGACATCTAGTCAGAGTCTTACATAGTATGGAACACCTATTGAAATGG 177
QY 181 TACCTGCAGAAAGCTGCGCAGTCTCCACAGCTCTCATCTATGAGATTCCAAAGATT 240
Db 178 TACCTGCAGAAAGCTGCGCAGTCTCCAAAGCTCTCATCTATGGAATTCATCCGATT 237
QY 241 TCTGGGGGTCAGACAGGTCTAGTGGCAGTCTTCCAGGACAGATTTACACTCAAGATC 300
Db 238 TCTGGGGTCCAGACAGGTCTAGTGGCAGTGGATCGAGACAGATTTACACTCAATATC 297
QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTATTACTGCTTACAGATTCACATCAGCCG 360
Db 298 AGCAGAGTGGAGGCTGAGAGTCTGGGAATTTACTGCTTCAAGGTTCCATGTTCCG 357
QY 361 TACAGGTTGGAGGAGGACCAAGGTGGAATTAAC 397
Db 358 TACAGGTTGGAGGAGGACCAAGCTGGAATTAAC 394

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RESULT 15
062788 standard; CDNA: 394 BP.

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AC 062788;
DT 24-JAN-1995 (first entry)
DE Murine KC-4 immunoglobulin light chain variable region CDNA.
KW Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human milk fat globule; human breast carcinoma;
OS Mus musculus.
FH Key 1 Location/Qualifiers
FT cds 1..393
FT mat_peptide /tag=8
FT /note="KC-4 VL chain (no termination codon)"
FT /tag=58..393
FT /product="light_chain_V-region"
PN M09411509-A.
PD 26-MAY-1994.
PE 16-NOV-1993; U11445.
PR 16-NOV-1992; US-977696.
PR 30-SEP-1993; US-129930.
PR 08-OCT-1993; US-134346.
PA (CANC-) CANCER RES FUND CONTRA COSTA.
PI Ceriani RL, Do Couto FJR, Padian EA, Peterson JA;
DR WPI; 94-183510/22.
PT New analogue peptide(s) comprising antibody variable regions -
PT used to develop prods. for use in the detection, diagnosis,
PT therapy and prevention of neoplasms.
PS Example 25; Page 60; 109pp; English.
CC An initial isolation of cDNAs coding for murine anti-human breast
CC carcinoma MAb KC-4 was performed using PCR with commercially
CC available primers (see 062776-062783, available from NOVAGEN).
CC Subsequent cloning using PCR primers J020, J021, J022 and J024
CC (see 062784-062787) resulted in the isolation of the mouse Ig
CC variable domains. The amplified cDNAs were sequenced (062788 and
CC 062789). Chimeric mouse-human antibodies were constructed
CC using human constant regions so as to produce less immunogenic
CC polypeptides which retained the anti-human carcinoma binding
CC specificity of KC-4.
SQ Sequence 394 BP; 98 A; 91 C; 96 G; 109 T;

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Query Match 69.4%; Score 286.6; DB 1; Length 394;

Best Local Similarity 84.4%; Pred. No. 6.1e-86;

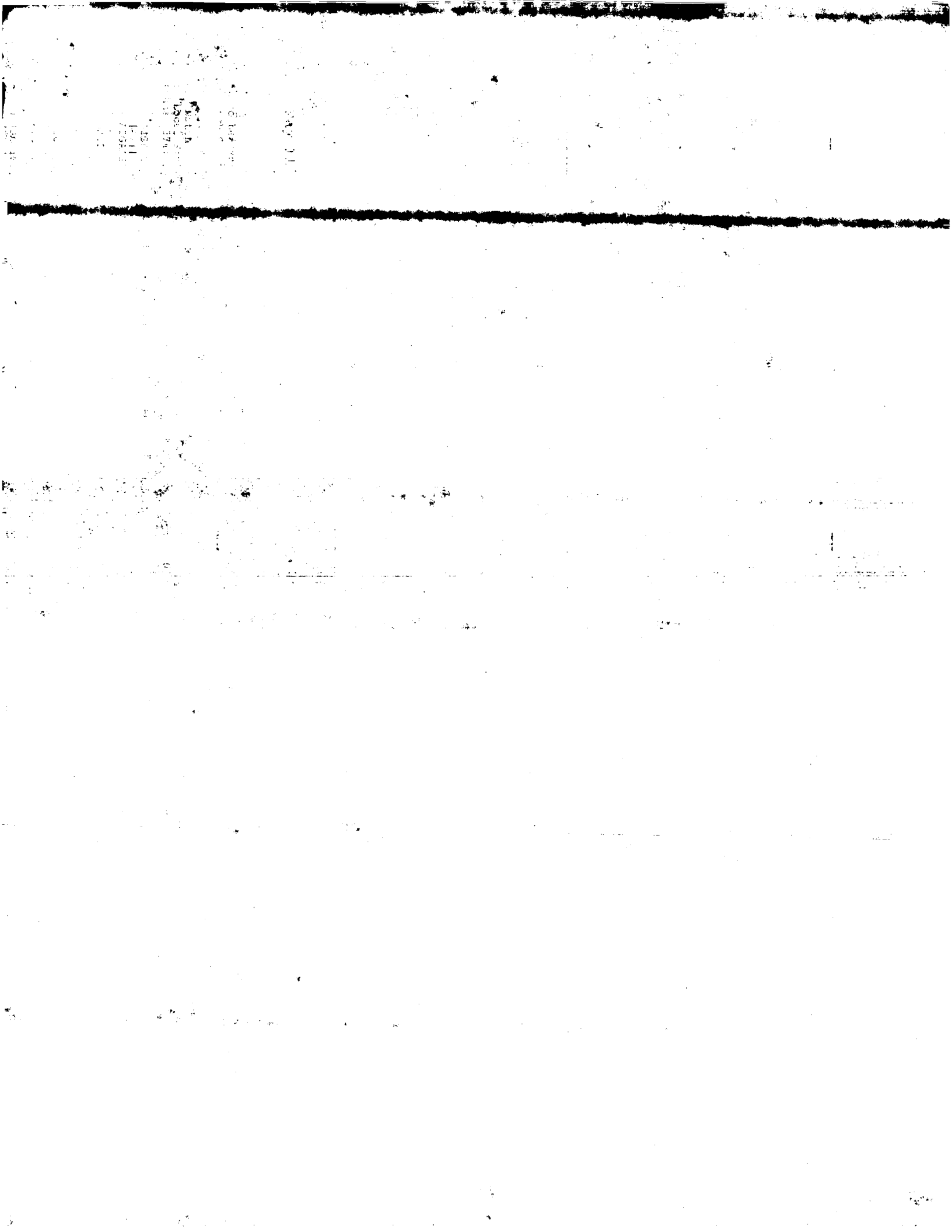
Matches 335; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

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Db 1 ATGAAGTTCCTGTTAGGCTGTGTGTC---CTGATGTTTCGATTCCTGCTTCCAGCAGT 57
QY 61 GATGTTTGATGATCAACCAAGTCAACTCTCCCTGCTGTCACCCCTGGAGAACAGCTTCT 120
Db 58 GATGTTTGATGATCAACCAAGTCAACTCTCCCTGCTGTCACCCCTGGAGAACAGCCTCC 117
QY 121 ATCTCTGACAGGTCTAGTCAGAGTCTTCCAAAGATTTGGGAACACCTATTGCTTGG 180
Db 118 ATCTCTGACATCTAGTCAGAGTCTTACATAGTATGGAACACCTATTGAAATGG 177
QY 181 TACCTGCAGAAAGCTGCGCAGTCTCCACAGCTCTCATCTATGAGATTCCAAAGATT 240
Db 178 TACCTGCAGAAAGCTGCGCAGTCTCCAAAGCTCTCATCTATGGAATTCATCCGATT 237
QY 241 TCTGGGGTCCAGACAGGTCTAGTGGCAGTGGATCGAGACAGATTTACACTCAAGATC 300
Db 238 TCTGGGGTCCAGACAGGTCTAGTGGCAGTGGATCGAGACAGATTTACACTCAATATC 297
QY 301 TCGGAGTAGAGGCTGAGAGCTGGAGTATTACTGCTTACAGATTCACATCAGCCG 360
Db 298 AGCAGAGTGGAGGCTGAGAGTCTGGGAATTTACTGCTTCAAGGTTCCATGTTCCG 357
QY 361 TACAGGTTGGAGGAGGACCAAGGTGGAATTAAC 397
Db 358 TACAGGTTGGAGGAGGACCAAGCTGGAATTAAC 394

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Search completed: May 11, 1999, 12:03:37
Job time: 1544 sec




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DB 1 MRLPQALLGLMLMWPVSGSDVYMTQSPSLPYTPGEPASISCRSSQSLVSDGNTHLW 60
QY 61 YLQKPGQSPQQLLYIGISNRFSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCLQGTQHP 120
DB 61 FQQRPGQSPRLIYKYNRDSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCMQGTQHP 120
QY 121 YTFGGGTKEIKR 133
DB 121 YTFGGGTKEIKR 133

RESULT 3
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998
C:Accession: B32513
R:Kofler, R.; Strahel, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOF>
A:Cross-references: GB:M20828; NID:9196937; PID:9196938
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

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```

Query Match 77.2%; Score 555.5; DB 2; Length 131;
Best Local Similarity 81.8%; Pred. No. 3.2e-43;
Matches 108; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

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```

QY 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLVHSGNTYLSW 59
QY 61 YLQKPGQSPQQLLYIGISNRFSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCLQGTQHP 120
DB 61 YLQKPGQSPRLIYKYNRDSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCMQGTQHP 119
QY 121 YTFGGGTKEIKR 132
DB 121 YTFGGGTKEIKR 131

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RESULT 4
K2HURP
Ig kappa chain precursor V-II region (RPM1) - human

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C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combario, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6439-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852
A:Accession: A01890
A:Molecule type: DNA
A:Residues: 1-133 <KLO>
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-133/Product: Ig kappa chain V-II region (RPM1) #status predicted <MAT>
F:21-43/Region: framework 1

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F:36-115/Domain: Immunoglobulin homology <IMN>
F:44-59/Region: complementarity-determining 1
F:60-74/Region: framework 2
F:75-81/Region: complementarity-determining 2
F:82-113/Region: framework 3
F:114-122/Region: complementarity-determining 3
F:123-133/Region: framework 4
F:43-113/Disulfide bonds: #status predicted

```

```

Query Match 77.1%; Score 555; DB 1; Length 133;
Best Local Similarity 79.7%; Pred. No. 3.6e-43;
Matches 106; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

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```

QY 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLVSDGNTHLW 60
QY 61 YLQKPGQSPQQLLYIGISNRFSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCLQGTQHP 120
DB 61 FQQRPGQSPRLIYKYNRDSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCMQGTQHP 120
QY 121 YTFGGGTKEIKR 133
DB 121 YTFGGGTKEIKR 133

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RESULT 5
B30577

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Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C:Species: Mus musculus (house mouse)

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```

C>Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C:Accession: B30577
R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th
J. Exp. Med. 161, 805-815, 1985
A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r
A:Reference number: A30577; MUID:85159423
A:Accession: B30577
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <KOF>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

```

```

Query Match 76.9%; Score 553.5; DB 2; Length 131;
Best Local Similarity 81.1%; Pred. No. 4.8e-43;
Matches 107; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

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```

QY 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MRLPYRLVLLFLFWIPVSGDVYMTQSPSLPYTPGEPASISCRSSQSLVHSGNTYLSW 59
QY 61 YLQKPGQSPQQLLYIGISNRFSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCLQGTQHP 120
DB 61 YLQKPGQSPRLIYKYNRDSGVDPDRFSGSGSTDTFTLKISRVEADGVYVYCMQGTQHP 119
QY 121 YTFGGGTKEIKR 132
DB 121 YTFGGGTKEIKR 131

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RESULT 6
B25912

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```

Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)

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C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Mar-1998
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912

```

RESULT 8
D34904
Ig kappa chain precursor V region (3-13) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 20-Mar-1998
C:Accession: D34904
R:Bedzyk, R.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive
A:Reference number: A34903; MUID:90094387
A:Accession: D34904

```

RESULT 10
S22902
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S22902
R:Chastagner, P.; Theze, J.; Zouali, M.
Gene 101, 305-306, 1991
A:Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region
A:Reference number: S22902; MIMD:11276285
A:Accession: S22902
A:Status: preliminary; translation not shown

```

C; Date: 23-Jan-1998
C; Accession: S22658

```

0y  61 YLQPGQSPOLLITYGISNRFEGVPPDRFSGSGSTDFTLKISRVEADGVYYCLOGTHQ 120
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  61 FQQRPGQSPRLITYKSNRDSGVPPDRFSGSGSTDFTLKISRVEADGVYYCMQGTHTS 120

```

Tue May 11 13:50:15 1999

us-08-700-737-21.rpt

Page 5

```
QY 121 YTFGGGCTKVEIKR 133
      :| | | | | | | | | |
Db 121 WTFGGGCTKVEIKR 133
```

RESULT 14

Ig kappa chain precursor V region (10-25) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 20-Mar-1998
C:Accession: G34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive murine anti-ovalbumin antibody
A:Reference number: A34903; MUID:90094387
A:Accession: G34903
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BBS>
A:Cross-references: GB:M32381; GB:J05237; GB:J05238; NID:639654; PID:639655
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match	75.3%	Score 542.5	DB 2	Length 131
Best Local Similarity	79.5%	Pred No. 4.6e-42		
Matches 105	Conservative 10	Mismatches 16	Indels 1	Gaps 1

```

Oy      1 MKLPVRLVLLFWIPVSGGDVYNTQSPLESLPVTTCGPASISCRSSQSGLAKSYGNTYLSW 600
        ||||| :||| | |||||:||||| :| ||||| ||||| |
Db      1 MKLPVRLV-LFWIPASSSDVYNTQTPLSLPVSLGQASISCRSSQSGLHNGNTYFHW 599

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```

Oy 61 YLQRPQSPOLLITYGISNRFSGVDRFSGSGGTFTLKISRVEADVGYYVCLQGTTHQ 120
      |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 YLQRPQSPOLLITKYNSRFSGVDRFSGSGGTFTLKISRVEADLDGVYFCSQSTHP 119

```

```
QY      121 YTFGGSTKVEIK 132
        ||| |||::|
Db      120 LTFGAGTKLELK 131
```

RESULT 15

anti-digoxin transfectoma antibody heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Sep-1998 #sequence_revision 03-Sep-1998 #text_change 03-Sep-1998
C:Accession: PH0106
R:Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolles, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A:Reference number: PH0105; MUID:91015092
A:Accession: PH0106
A:Status: preliminary
A:Residues: 1-132 <NEA>

Query Match	75.3%	Score 542.5	DB 3	Length 132
Best Local Similarity	79.7%	Pred. No. 4.7e-42		
Matches 106	Conservative 11	Mismatches 15	Indels 1	Gaps 1

```

Oy      1 MKLPVRLVLLFWIPVSGGDVVMQSP.LPVTGPEPASISCRSSQSGLAKSYGNMYLSW 600
          ||||| :||| :||||:||||: |:||||| ||| :|||:|
Db      1 MKLPVRLVLLFWIPVSGGDVVMQTP.LSLPVSGLQASISCRSSQSGLVHNSGNTYLLNW 599

```

QY 61 YLAKPGQSPOLLITYGISNRFSGVDPDRFSGSGGTFTLKISRVEADVGYYCYCLOGTHQP 120

Db 60 YLQAGQSFKLLITYKSNRFSGVDPDRFSGSGGTFTLKISRVEADLGITFCSQTHVP 119

QY	121	YTFGQGTKEIKR	133
		:	
Db	120	PTFGGCTKEIKR	132

```
Search completed: May 11, 1999, 12:23:25
Job time: 298 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:20:08 ; Search time 22.45 Seconds

(without alignments)
164.987 Million cell updates/sec

Title: US-08-700-737-21

Perfect score: 720
Sequence: 1 MKLPVRLVLLFWIPVSGG.....QPTFGQGTKEIKRADAP 138

Scoring table: BLOSUM62

Searched: 74019 seqs, 26840295 residues

Database: SwissProt_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	77.1	133	1	KV2E_HUMAN
2	501	69.6	117	1	KV2E_HUMAN
3	491	68.2	113	1	KV2D_HUMAN
4	479.5	66.6	115	1	KV2A_HUMAN
5	473	65.7	113	1	KV2G_MOUSE
6	466	64.7	113	1	KV2B_HUMAN
7	453.5	63.0	112	1	KV2C_HUMAN
8	440	61.1	129	1	KV3M_HUMAN
9	439	61.0	129	1	KV3M_HUMAN
10	428	59.4	113	1	KV2E_MOUSE
11	422	58.6	113	1	KV2E_MOUSE
12	420	58.3	112	1	KV2D_MOUSE
13	419.5	58.3	134	1	KV4C_HUMAN
14	417	57.9	129	1	KV3H_HUMAN
15	415.5	57.7	128	1	KV3K_HUMAN
16	408.5	56.7	108	1	KV1_CANFA
17	397	55.1	133	1	KV4B_HUMAN
18	393.5	54.7	131	1	KV3I_MOUSE
19	393	54.6	120	1	KV2B_MOUSE
20	391.5	54.4	132	1	KV3F_MOUSE
21	391	54.3	113	1	KV2C_MOUSE
22	384	53.3	122	1	KV2A_MOUSE
23	384	53.3	109	1	KV3B_HUMAN
24	382.5	53.1	114	1	KV4A_HUMAN
25	375	52.1	109	1	KV3D_HUMAN
26	372	51.7	108	1	KV3A_HUMAN
27	371	51.5	109	1	KV3E_HUMAN
28	370	51.4	109	1	KV3F_HUMAN
29	369.5	51.3	115	1	KV3I_HUMAN
30	367.5	51.0	111	1	KV3H_MOUSE
31	363	50.4	109	1	KV3G_HUMAN
32	361.5	50.2	136	1	KV5B_MOUSE
33	357.5	49.7	111	1	KV3L_MOUSE
34	356.5	49.5	111	1	KV3J_MOUSE
35	355.5	49.4	111	1	KV3M_MOUSE
36	355.5	49.4	121	1	KV4O_HUMAN
37	353.5	49.1	128	1	KV5O_MOUSE
38	352.5	49.0	111	1	KV3O_MOUSE
39	352	48.9	116	1	KV3J_HUMAN
40	348.5	48.4	129	1	KV4I_HUMAN
41	348.5	48.4	111	1	KV3N_MOUSE
42	347.5	48.3	111	1	KV3K_MOUSE
43	347.5	48.3	111	1	KV3O_MOUSE

ALIGNMENTS

RESULT	1	2
KV2E_HUMAN	STANDARD;	PRT; 133 AA.
ID	KV2E_HUMAN	
AC	P06310	
DT	01-JAN-1988 (REL. 06, CREATED)	
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)	
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)	
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (RPMI 6410).	
OS	HOMO SAPIENS (HUMAN)	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 86041852.	
RA	KLOBECK H.G., MEINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;	
RL	NUCLEIC ACIDS RES. 13:6499-6513(1985).	
DR	EMBL; 200020; G296655; -.	
DR	PIR; A01890; K2HURP.	
DR	HSSP; P01607; 4FAB.	
KW	IMMUNOGLOBULIN V REGION; SIGNAL.	
FT	SIGNAL	1 20
FT	CHAIN	21 133
FT	DOMAIN	21 43
FT	DOMAIN	44 59
FT	DOMAIN	60 74
FT	DOMAIN	75 81
FT	DOMAIN	82 113
FT	DOMAIN	114 122
FT	DOMAIN	123 132
FT	DISULFID	43 113
FT	NON_TER	133 133
SO	SEQUENCE	133 AA; 14707 MW; 2DC342B5 CRC32;
Query Match		
Best Local Similarity		
Matches 106; Conservative 79.7%; Pred. No. 6.4e-47; Mismatches 15; Indels 0; Gaps 0;		
QY	1 MKLPVRLVLLFWIPVSGGVMTOSPLPYTPGEPAISICRSQSIAKSYGNTYISW 60	
DB	1 MRLPAQLGLMLMWPGSSGDVMTQSPISLPVTLGQPASICRSQSIVYSGNTYLNW 60	
QY	61 YLQKPGSPOLLITGYSNFGSVDPDRFGSGGTDTLKSIVAEADGVYVCIQGTQP 120	
DB	61 FQDRPGQSPRLITKVSNDGVPDRFGSGGTDTLKSIVAEADGVYVCIQGTQHS 120	
QY	121 YTFGGGTKEIKR 133	
DB	121 WTEGGGTKEIKR 133	
RESULT 2		
ID	KV2E_HUMAN	STANDARD; PRT; 117 AA.
AC	P06309	
DT	01-JAN-1988 (REL. 06, CREATED)	
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)	
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (GM607) (FRAGMENT).	
OS	HOMO SAPIENS (HUMAN)	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 84191506.	
RA	KLOBECK H.G., SOLOMON A., ZACHAU H.G.;	

RX MEDLINE; 83178921.
RA NOVOTNY J., MARGOLIES M.N.;
RL BIOCHEMISTRY 22:1153-1158(1983).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA PROTEIN THAT
CC BINDS DIGOXIN.
DR PIR; A01914; KWS26.
HSP; P01607; 11GT.
KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
FT DOMAIN 1 23
FT DOMAIN 2 39
FT DOMAIN 3 40
FT DOMAIN 4 54
FT DOMAIN 5 55
FT DOMAIN 6 61
FT DOMAIN 7 62
FT DOMAIN 8 93
FT DOMAIN 9 94
FT DOMAIN 10 102
FT DOMAIN 11 112
FT DISULFID 23 93
FT NON_TER 113
SQ SEQUENCE 113 AA; 12273 MW; 58372CBE CRC32;

Query Match 65.7%; Score 473; DB 1; Length 113;
Best Local Similarity 80.5%; Pred. No. 4,2e-39;
Matches 91; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 21 DVVMTQSPISLPYPGEPASISCRSSQSLAKSYGNTYLSWYLRQSGSPOLLIGISNRF 80
DB 1 DVVMTQSPISLPYSLGDPASISCRSSQSLVHNGNTYLNWYLRQSGSPOLLIGISNRF 60
QY 81 SGVDFRSGSGSDFTFLKISRVAEDVGYCCLOGTHOPTFGGQTVKRIK 133
DB 61 SGVDFRSGSGSDFTFLKISRVAEDGIFYCQTHVPTFGGQTVKRIK 113

RESULT 6
KV2L_HUMAN STANDARD; PRT; 113 AA.
ID P01615;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (FR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE; 76253627.
RA RIESEN W.F., JATON J.-C.;
RL BIOCHEMISTRY 15:3829-3833(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUF.
HSP; P01607; 1TEL.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 2 39
FT DOMAIN 3 40
FT DOMAIN 4 54
FT DOMAIN 5 55
FT DOMAIN 6 61
FT DOMAIN 7 62
FT DOMAIN 8 93
FT DOMAIN 9 94
FT DOMAIN 10 102
FT DOMAIN 11 112
FT DISULFID 23 93
FT NON_TER 113
SQ SEQUENCE 113 AA; 12660 MW; 53CADDE CRC32;

Query Match 64.7%; Score 466; DB 1; Length 113;
Best Local Similarity 79.6%; Pred. No. 2e-38;
Matches 90; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 21 DVVMTQSPISLPYPGEPASISCRSSQSLAKSYGNTYLSWYLRQSGSPOLLIGISNRF 80
DB 1 DVVMTQSPISLPYSLGDPASISCRSSQSLVHNGNTYLNWYLRQSGSPOLLIGISNRF 60

QY 81 SGVDFRSGSGSDFTFLKISRVAEDVGYCCLOGTHOPTFGGQTVKRIK 133
DB 61 SGVDFRSGSGSDFTFLKISRVAEDVGYCCLOGTHOPTFGGQTVKRIK 113

RESULT 7
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID P01616;
AC 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-II REGION (MIL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RA DREYER W.J., GRAY W.R., HOOD L.E.;
RL COLD SPRING HARB. SYMP. QUANT. BIOL. 37:353-367(1967).
CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- THIS IS A BENGE-JONES PROTEIN.
DR PIR; A01887; K2HOML.
HSP; P01679; 1CBV.
KW IMMUNOGLOBULIN V REGION; BENGE-JONES PROTEIN.
FT DOMAIN 1 23
FT DOMAIN 2 38
FT DOMAIN 3 39
FT DOMAIN 4 53
FT DOMAIN 5 54
FT DOMAIN 6 60
FT DOMAIN 7 61
FT DOMAIN 8 91
FT DOMAIN 9 92
FT DOMAIN 10 101
FT DOMAIN 11 111
FT DISULFID 23 92
FT NON_TER 112
SQ SEQUENCE 112 AA; 12055 MW; C487DFDE CRC32;

Query Match 63.0%; Score 453.5; DB 1; Length 112;
Best Local Similarity 75.2%; Pred. No. 3,2e-37;
Matches 85; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

QY 21 DVVMTQSPISLPYPGEPASISCRSSQSLAKSYGNTYLSWYLRQSGSPOLLIGISNRF 80
DB 1 DVVMTQSPISLPYSLGDPASISCRSSQSLVHNGNTYLNWYLRQSGSPOLLIGISNRF 60
QY 81 SGVDFRSGSGSDFTFLKISRVAEDVGYCCLOGTHOPTFGGQTVKRIK 133
DB 60 SGVDFRSGSGSDFTFLKISRVAEDVGYCCLOGTHOPTFGGQTVKRIK 112

RESULT 8
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID P18135;
AC 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (HAB).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 88171307.
RX KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RL J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOMANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P10022; K3HUBA.
HSP; P01607; 1AAG.
KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION (HAI).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129
 SO SEQUENCE 129 AA: 14073 MW: 2C44B85E CRC32:

Query Match 61.1%; Score 440; DB 1; Length 129;
 Best Local Similarity 63.2%; Pred. No. 7.4e-36;
 Matches 84; Conservative 22; Mismatches 23; Indels 4; Gaps 1;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLISLSPGERATLISCRASQSVSSS---YLAW 56
 OY 61 YLQKRGSPOLLIGISNRFSGVDPDRFSGSGGTDFLTLSRVEADGVYVYCCLOGTHP 120
 DB 57 YQKRGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTLSRLEPDEFAVYVYCCQYGTSP 116
 OY 121 YTFGGGTVEIKR 133
 DB 117 RTFGGGRVEIKR 129

RESULT 9
 ID KV3M_HUMAN STANDARD: PRT: 129 AA.
 AC P18136:
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (HIC).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 88171307.
 RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
 RL J. EXP. MED. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR: P10021; K3HUI.
 DR HSSP; P01607; IDPB.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129
 SO SEQUENCE 129 AA: 14070 MW: DD00C369 CRC32:

Query Match 61.0%; Score 439; DB 1; Length 129;
 Best Local Similarity 62.4%; Pred. No. 9.3e-36;
 Matches 83; Conservative 23; Mismatches 23; Indels 4; Gaps 1;

DB 1 METPAQLFLLLMLPDTGTEIVLTQSPGTLISLSPGERATLISCRASQSVSSS---YLAW 56
 OY 61 YLQKRGSPOLLIGISNRFSGVDPDRFSGSGGTDFLTLSRVEADGVYVYCCLOGTHP 120
 DB 57 YQKRGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTLSRLEPDEFAVYVYCCQYGTSP 116
 OY 121 YTFGGGTVEIKR 133
 DB 117 RTFGGGRVEIKR 129

RESULT 10
 ID KV2E_MOUSE STANDARD: PRT: 113 AA.
 AC P01630:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (7S34.1).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 83256427.
 RA CHANG J.-Y., HERBST H., AEBERSOLD R., BRAUN D.G.;
 RL BIOCHEM. J. 211:173-180(1983).
 CC -I- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
 AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR: A01913; KMS75.
 DR HSSP; P01679; ICGS.
 KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113
 SO SEQUENCE 113 AA: 12496 MW: AE067DC8 CRC32:

Query Match 59.4%; Score 428; DB 1; Length 113;
 Best Local Similarity 74.3%; Pred. No. 9.1e-35;
 Matches 84; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 21 DVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSWTLQKRGSPOLLIGISNRF 80
 DB 1 DIVMTQSPILSPVTPGEPASISCRSSQSLAKSYGNTYLSWTLQKRGSPOLLIGISNRF 80
 OY 81 SGVDPDRFSGSGGTDFLTLSRVEADGVYVYCCLOGTHPPTFGGTVEIKR 133
 DB 61 SGVDPDRFSGSGGTDFLTLSRVEADGVYVYCCQYGTSPPTFGGTVEIKR 113

RESULT 11
 ID KV2E_MOUSE STANDARD: PRT: 113 AA.
 AC P03976:
 DT 23-OCT-1986 (REL. 02, CREATED)
 DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (17S29.1).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 85128968.
 RA AEBERSOLD R., HERBST H., GRUTTER T., CHANG J.Y., BRAUN D.G.;

RL HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 365:1375-1383(1984).
 CC -1- ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
 DR PIR; A01912; KMS17.
 KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 FRAMEWORK 2.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12390 MW; 6A4522AE CRC32;

Query Match 58.6%; Score 422; DB 1; Length 113;
 Best Local Similarity 74.3%; Pred. No. 3.5e-34;
 Matches 84; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

OY 21 DVTMTQSPSLPVTGPEPASISCRSSQSLAKSYGNTYLSMYLQKPGSPOLLIGYSNRF 80
 DB 1 DVTMTQAFNSNPNVLTGTSASISCRSSKSLHNGITYLYLQKPGSPOLLIGYSNLA 60
 OY 81 SGVDPFSGSGSGDTFTLKISRVEADVGVYVYCLOGTHQPTFGGTKEIKR 133
 DB 61 SGVDPFSGSGSGDTFTLKISRVEADVGVYVYCAHLELPTFGGTKEIKR 113

RESULT 12
 KV2D_MOUSE STANDARD; PRT; 112 AA.
 ID KV2D_MOUSE
 AC P01629;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-II REGION (251.3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 83055101.
 RA HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 363:1069-1076(1982).
 CC -1- THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY
 CC AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR; A01911; KMS1.
 KW HSSP; P01607; 4FAB.
 RN IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 FRAMEWORK 2.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12221 MW; C16DB265 CRC32;

Query Match 58.3%; Score 420; DB 1; Length 112;
 Best Local Similarity 75.0%; Pred. No. 5.3e-34;
 Matches 84; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

OY 21 DVTMTQSPSLPVTGPEPASISCRSSQSLAKSYGNTYLSMYLQKPGSPOLLIGYSNRF 80
 DB 1 DVTMTQAFNSNPNVLTGTSASISCRSSKSLHNGITYLYLQKPGSPOLLIGYSNLA 60
 OY 81 SGVDPFSGSGSGDTFTLKISRVEADVGVYVYCLOGTHQPTFGGTKEIKR 132
 DB 61 SGVDPFSGSGSGDTFTLKISRVEADVGVYVYCAHLELPTFGGTKEIKR 112

DB 61 SGVDPFSGSGSGDTFTLKISRVEADVGVYVYCAHLELPTFGGTKEIKR 112

RESULT 13

KV4C_HUMAN STANDARD; PRT; 134 AA.
 ID KV4C_HUMAN
 AC P06314;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-IV REGION (B17).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86041854.
 RA MARSH P., MILLS F., GOULD H.;
 RL NUCLEIC ACIDS RES. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA MARSH P.;
 RL SUBMITTED (OCT-1985) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR PIR; A01905; K4H017.
 DR HSSP; P01607; 21MN.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-III REGION (B17).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 FRAMEWORK 3.
 FT DOMAIN 122 133 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 132 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; BB63E06A CRC32;

Query Match 58.3%; Score 419.5; DB 1; Length 134;
 Best Local Similarity 64.2%; Pred. No. 7.3e-34;
 Matches 86; Conservative 16; Mismatches 31; Indels 1; Gaps 1;

OY 1 MKLPRLVLLFWTPGSGGVYVYVYCLOGTHQPTFGGTKEIKR 59
 DB 1 MYLQTVFTSLTLMTSGAVGDIWMTQSPSLAVSLGERATTNCKSSOSILYSSDKRYLA 60
 OY 60 WTLQKPGSPOLLIGYSNRFSGVDPDRFSGSGSGDTFTLKISRVEADVGVYVYCLOGTHQ 119
 DB 61 WTLQKPGSPOLLIGYSNRFSGVDPDRFSGSGSGDTFTLKISRVEADVGVYVYCLOGTHQ 120
 OY 120 PYTFGSGTKEIKR 133
 DB 121 PYTFGSGTKEIKR 134

RESULT 14
 KV3H_HUMAN STANDARD; PRT; 129 AA.
 ID KV3H_HUMAN
 AC P04207;
 DT 20-MAR-1987 (REL. 04, CREATED)
 DT 01-NOV-1980 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-III REGION (CLL) (RHEUMATOID FACTOR).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 86177570.
 RA JIRIK F.R., SORGE J., FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,

RA GOLDFIEB R., CARSON D.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986).
DR EMBL: M12740; G553486; -
DR PIR: A01898; K3HCL.
DR HSSP: P01607; 1ANG.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 1 129 IG KAPPA CHAIN V-III REGION (CLL).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 119 129 JK1 SEGMENT.
FT NON_TER 43 108 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14275 MW; 2F344868 CRC32;

Query Match Best Local Similarity 57.9%; Score 417; DB 1; Length 129;
Matches 80; Conservative 24; Mismatches 24; Indels 6; Gaps 2;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPVLPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MEAPQALLFLLLMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSN-----LAW 55
OY 61 YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGGTDFTLKISRVEADGVYVYCCLOGTHQ 119
DB 56 YQKRGQSPRLIRDPASSRANGIPDRFSGSGGTDFTLKISRLEPEDFAVYVYCCQYSTSP 115
OY 120 PYFGGQTVETIKR 133
DB 116 PWTFGGTVETIKR 129

RESULT 15
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041852.
RA KLOBECK H.G., MEINDL A., COMBIATO G., SOLOMON A., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR EMBL: 200021; G33179; -
DR PIR: A01899; K3H041.
DR HSSP: P01607; 3HEM.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 20
FT CHAIN 1 128 IG KAPPA CHAIN V-III REGION (IARC/BL41).
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 118 128 JK1 SEGMENT.
FT NON_TER 43 108 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14070 MW; 318E08AF CRC32;

Query Match Best Local Similarity 57.7%; Score 415.5; DB 1; Length 128;
Matches 80; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

OY 1 MKLPVRLVLLFWIPVSGDVMTQSPVLPVTPGEPASISCRSSQSLAKSYGNTYLSW 60
DB 1 MEAPQALLFLLLMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSN-----LAW 55
OY 61 YLQKPGQSPQLLYIGISNRFSGVDPDRFSGSGGTDFTLKISRVEADGVYVYCCLOGTHQ 120
DB 56 YQKRGQSPRLIRDPASSRANGIPDRFSGSGGTDFTLKISRLEPEDFAVYVYCCQYSTSP 115
OY 121 YTFGGQTVETIKR 133
DB 116 YTFGGQTVETIKR 128

Search completed: May 11, 1999, 12:20:09
Job time: 306 sec

OM protein - protein search, using sw model

Run on: May 11, 1999, 12:21:01 ; Search time 38.54 Seconds
(without updates)

(without alignments)
197.544 Million cell updates/sec

Title: US-08-700-737-21

Sequence: 1 MKLPVRLVLLFWIPVSGG.....QPYTEGGQGTKEIKRADAAP 138

Scoring table: BLOSUM62

Searched: 180763 seqs, 55169189 residues

Database :

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1:  SPTRMBL:.*
2:  sp_fungi:.*
3:  sp_funaria:.*
4:  sp_invertebrate:.*
5:  sp_mammal:.*
6:  sp_mhc:.*
7:  sp_ornanlele:.*
8:  sp_phase:.*
9:  sp_plant:.*
10: sp_bacteria:.*
11: sp_rudent:.*
12: sp_virus:.*
13: sp_unclassified:.*
14: sp_archaea:.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Query Score	Match Length	DB	ID	Description
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1	427	59.3	100	2	Q15535	Q15535 homo sapien
2	312	43.3	130	10	P80913	P80913 mus musculus
3	133	18.5	513	10	P97797	P97797 mus musculus
4	131.5	18.3	50	2	Q15533	Q15533 homo sapien
5	131	18.2	123	10	Q61243	Q61243 mus musculus
6	131	18.2	509	10	O08907	O08907 mus musculus
7	130	18.1	132	5	Q31175	Q31175 mus musculus
8	129	17.9	509	10	O35924	O35924 mus musculus
9	127.5	17.7	135	5	Q31174	Q31174 mus musculus
10	127	16.9	509	10	O88555	O88555 mus musculus
11	122	16.7	291	10	O88556	O88556 mus musculus
12	114.5	15.9	145	2	Q16237	Q16237 homo sapien
13	114.5	15.9	228	10	Q70153	Q70153 rattus norv
14	112.5	15.6	132	5	Q31177	Q31177 mus musculus
15	111.5	15.5	118	5	Q31176	Q31176 mus musculus
16	109	15.1	133	5	Q31178	Q31178 mus musculus
17	108.5	15.1	1021	2	Q15856	Q15856 homo sapien
18	108.5	15.1	1021	2	Q93033	Q93033 homo sapien
19	108	15.0	506	4	Q46632	Q46632 bos taurus
20	107.5	14.9	135	2	Q99602	Q99602 homo sapien
21	105.5	14.7	509	10	P97710	P97710 rattus norv
22	104.5	14.5	503	2	P78324	P78324 homo sapien
23	104	14.4	134	5	Q31180	Q31180 mus musculus
24	102.5	14.2	210	4	P79336	P79336 felis silve
25	102	14.2	506	4	Q46631	Q46631 bos taurus
26	101.5	14.1	418	10	Q70426	Q70426 rattus norv
27	101	14.0	137	5	Q31181	Q31181 mus musculus
28	100.5	14.0	252	12	Q90566	Q90566 glinglymstoc
29	99.5	13.8	358	2	O00241	O00241 homo sapien

30	99.5	13.8	700	2	075054	075054	homo sapien
31	99	13.8	198	2	Q13970	Q13970	homo sapien
32	95.5	13.3	133	12	Q90553	Q90553	ginglymost
33	94.5	13.3	254	12	Q90557	Q90557	ginglymost
34	94.5	13.1	119	2	Q99599	Q99599	homo sapien
35	94.5	13.1	121	2	Q99600	Q99600	homo sapien
36	94	13.1	122	2	Q99603	Q99603	homo sapien
37	94	13.1	157	12	Q90539	Q90539	ginglymost
38	93	12.9	122	2	Q99604	Q99604	homo sapien
39	91	12.6	145	12	Q90555	Q90555	ginglymost
40	90.5	12.6	288	2	Q00517	Q00517	homo sapien
41	90	12.5	120	5	Q31212	Q31212	mus musculu
42	90	12.5	117	10	Q61863	Q61863	mus muscul
43	90	12.5	143	12	Q90537	Q90537	ginglymost
44	89	12.4	1273	3	Q44928	Q44928	caenorhabdi
45	89	12.4	423	3	P91572	P91572	caenorhabdi

RESULT	1			
015535				
ID	015535	PRELIMINARY;	PRT;	100 AA.
AC	015535;			
DT	01-NOV-1996	(TREMBLREL, 01, CREATED)		
DT	01-NOV-1996	(TREMBLREL, 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998	(TREMBLREL, 08, LAST ANNOTATION UPDATE)		
DE	V KAPPA (FRAGMENT) .			
OS	HOMO SAPIENS (HUMAN) .			
OC	EUROARCTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES			
CC	CANARHINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	KATO S., TACHIBANA K., TAKAYAMA N., KATOKA H., YOSHIDA M.C.,			
RA	TAKANO T.;			
RL	SUBMITTED (SEP-1990) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL; D90161; G1262585; -.			
PFAM;	P00047; 1g; 1.			
FT	NON_TER	1		
FT	NON_TER	100	100	
SEQUENCE	100 AA;	10871 MW;	06A1440D	CRC32;

Query Match	59.3%;	Score 427;	DB 2;	Length 100;
Best Local Similarity	83.0%;	Pred. No. 3.6e-32;		
Matches	83;	Conservative	6;	Mismatches 11;
			Indels	0;
			Gaps	0;

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Oy 21 DVMVTSGLPLPTPEEPSPISCRSSSSIAKSYGNTYTSWTLKPGSGPOLLIYGISNR 80
Db 1 DVMVTSGLPLSLTTPGQPSISCRKSIQSLSHBDGNTIYXLYLQKPGSGPOLLIYESSR 60
Oy 81 SGVPDRFSGSGSCTDTLKISRVEADNGVYVYCLDGTQP 120
Db 61 SGVPDRFSGSGSCTDTLKISRVEADNGVYVYCMGILP 100

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RESULT      2
P80913
ID    P80913      PRELIMINARY;      PRT;      130 AA.
AC    P80913;
DT    01-NOV-1998 (TREMBLREL. 08, CREATED)
DT    01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT    01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE    IG KAPPA CHAIN V REGION PRECURSOR.
OS    MUS MUSCULUS (MOUSE).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA.
CC    SCURICOGNATHI; MORIDAE; MORINAE; MUS.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    JANON K.;
BL    SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR    EMBL; X79906; E269393; ALT_TERM.

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KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 130 IG KAPPA CHAIN V REGION.
 SQ SEQUENCE 130 AA; 14124 MW; 1DC6F7D9 CRC32;

Query Match 43.3%; Score 312; DB 10; Length 130;
 Best Local Similarity 50.0%; Pred. No. 1.4e-21;
 Matches 67; Conservative 18; Mismatches 43; Indels 6; Gaps 2;

QY 1 MKLPRLLVLLFWIPV--SGGDVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYL 58
 DB 1 MDFOVIFSLFLISASVMSRGQIVLTQSPALMSASISDERVTCTASSVSSS---YL 56
 QY 59 SWYLOKPGQSPOLLTYGINSNFGVDPDFSGSGSTDFTLKISRVEADVGYYCLOGTH 118
 DB 57 HWYQOKPSSPKWITSNLSASGVPAFSGSGSTSTSLTSSMEADDAITYCHQYHR 116
 QY 119 QPYTFGGQTKVEIK 132
 DB 117 FPHTEGGGTKEIK 130

RESULT 3

P97797 PRELIMINARY; PRT; 513 AA.

AC P97797; P97796;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE SHP SUBSTRATE-1 PRECURSOR (SHP-1) (SHP-1).

GN PTPNS1.

OS MUS MUSCULUS (MOUSE).

OC EUCAROTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCUROGNATHI; MORIDAE; MURINAE; MUS.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RA MEDLINE; 97223399.

RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,

RA FUJIOKA Y., KASUGA M.;

RT "Mouse and human SHP-1: molecular cloning of cDNAs and chromosomal

RT localization of genes."

RL BIOCHEM. BIOPHYS. RES. COMMUN. 231:61-67(1997).

CC -1- FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE

CC PHOSPHATASE 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY

CC VARIOUS MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN

CC AND INDUCE TRANSLLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA

CC MEMBRANE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN, ISOFORMS 1 AND 2,

CC ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE

CC SEQUENCE SHOWN HERE IS THAT OF ISOFORM 1.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.

DR EMBL; D87968; G1864015; -

DR EMBL; D87967; G1864013; -

DR MGD; MGI:108563; PTPNS1.

DR PPM; PFO0047; 1g; 3.

KW SIGNAL; TRANSMEMBRANE; ALTERNATIVE SPLICING; IMMUNOGLOBULIN FOLD;

KW GLYCOPROTEIN; SH3-BINDING; PHOSPHORYLATION.

FT CHAIN 1 27 513 SHP SUBSTRATE-1.

FT DOMAIN 27 373 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 374 394 POTENTIAL.

FT DOMAIN 395 513 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 51 124 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 167 234 IG-LIKE C1-TYPE DOMAIN.

FT DOMAIN 270 336 IG-LIKE C1-TYPE DOMAIN.

FT DOMAIN 440 443 SH2-BINDING (POTENTIAL).

FT DOMAIN 450 456 SH3-BINDING (POTENTIAL).

FT DOMAIN 464 467 SH2-BINDING (POTENTIAL).

FT DOMAIN 481 484 SH2-BINDING (POTENTIAL).

FT DOMAIN 505 508 SH2-BINDING (POTENTIAL).

FT MOD_RES 440 440 POTENTIAL.

FT MOD_RES 464 464 POTENTIAL.

FT MOD_RES 481 481 POTENTIAL.

FT MOD_RES 505 505 POTENTIAL.

FT CARBOHYD 54 54 POTENTIAL.

FT CARBOHYD 92 92 POTENTIAL.

FT CARBOHYD 168 168 POTENTIAL.

FT CARBOHYD 180 180 POTENTIAL.

FT CARBOHYD 205 205 POTENTIAL.

FT CARBOHYD 209 209 POTENTIAL.

FT CARBOHYD 246 246 POTENTIAL.

FT CARBOHYD 271 271 POTENTIAL.

FT CARBOHYD 293 293 POTENTIAL.

FT CARBOHYD 302 302 POTENTIAL.

FT CARBOHYD 312 312 POTENTIAL.

FT CARBOHYD 320 320 POTENTIAL.

FT CARBOHYD 345 345 POTENTIAL.

FT CARBOHYD 367 367 POTENTIAL.

FT VARSPLIC 425 428 MISSING (IN ISOFORM 2).

SQ SEQUENCE 513 AA; 56425 MW; 0F29251A CRC32;

Query Match 18.5%; Score 133; DB 10; Length 513;

Best Local Similarity 31.5%; Pred. No. 0.00011;

Matches 46; Conservative 25; Mismatches 53; Indels 22; Gaps 8;

QY 7 LTVLLV---FWIVSGDVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYL 62

DB 15 LCLLLASACCTGVTGKELKVTQPKERSVVAADSTVLNCTLTSLLPVG---PIKWY- 70

QY 63 QKPGSPOLLTYGINSN---FSGVDPDFSGSGSTDFTLKISRVEADVGYYCLO 115

DB 70 RGVGS-RLLISTGHEFPRTVVD--ATKRNMFISIRSVTEPDAGTYCVAFQK 126

QY 116 GTHQPYT---FGQTKVEIKRADAP 138

DB 127 GPSEPTEIQSGGTEYVLAKPSP 152

RESULT 4

ID Q15533 PRELIMINARY; PRT; 50 AA.

AC Q15533;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA

DE IN THE CELL LINE JI (CLONE JIP).

OS HOMO SAPIENS (HUMAN).

OC EUCAROTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;

OC CARNIVORINI; HOMINIDAE; HOMO.

RN [1]

RP SEQUENCE FROM N.A.

RA KLOBECK H.G.;

RL SUBMITTED (AUG-1987) TO EMBL/GENBANK/DBJ DATA BANKS.

RN [2]

RP SEQUENCE OF 36-50 FROM N.A.

RX MEDLINE; 87259967.

RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;

RT "kappa gene of a t(2;8) chromosomal translocation in a

RL NCLEIC ACIDS RES. 15:4877-4888(1987).

DR EMBL; X05929; E12675; -

SQ SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;

Query Match 18.3%; Score 131.5; DB 2; Length 50;

Best Local Similarity 48.1%; Pred. No. 1.3e-05;

Matches 25; Conservative 12; Mismatches 10; Indels 5; Gaps 1;

QY 21 DVMTQSPSLPTPEPPASISCRSSQSLAKSYGNTYLSWYLOKPGSPOLL 72


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DB 4 DIOMTQSPSSLSASVGDVATVISCQASQDI-----SNVLMWYQKPKAKRL 50
RESULT 5
ID 061243 PRELIMINARY: PRT: 123 AA.
AC 061243:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-B LYMPHOCYTE PROTEIN 3 (8S20 PROTEIN).
GN VPREB3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RC MEDLINE: 93259124.
RX SHIRASAWA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,
RA RAJWSKY K., TAKEFORI T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBL J 121827-1834(1993).
DR EMBL: D13208; G286065; -.
DR MGD: MGI:98938; VPREB3.
DR PFAM: PF00047; 19; 1.
FT CHAIN 20 123 8S20 PROTEIN.
SQ SEQUENCE 123 AA; 13400 MW; DA2A70D3 CRC32;

Query Match 18.2%; Score 131; DB 10; Length 123;
Best Local Similarity 35.3%; Pred. No. 3.8e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 8; Gaps 5;

QY 8 LVLLFWIVSGDVMTQSPVLSLPYPGEPAISCRSSQSLAKSYGNTYLSWTLQ 67
DB 7 LPLLIGTFVAVFQPTLL-PAFVSFPGQDAHLSCITNSQAHATA-GDIGVSYQOQPS 64
QY 68 SPOLLITVIGISN--RFSQVDPDRFSG--SGGTDFTLKISRVEADVGYVYC-LQGHOP 120
DB 65 AHHLYTYAEHEHYRPADIPDRFSATVDAAHNACILITISVLPEDDADYFCSTIAITFEP 123

RESULT 6
ID 008907 PRELIMINARY: PRT: 509 AA.
AC 008907:
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE BRAIN IMMUNOLOGICAL-LIKE WITH TYROSINE-BASED MOTIFS
DE (BIT, COMPLETE CDS).
GN BIT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RC MEDLINE: 97230468.
RX OHNISHI H., KUBOTA M., SANO S.;
RT "Bit (Bit) maps to mouse chromosome 2.";
RL GENOMICS 40:504-506(1997).
DR EMBL: D85785; D1021208; -.
DR MGD: MGI:107947; BIT.
DR PFAM: PF00047; 19; 3.
SQ SEQUENCE 509 AA; 56033 MW; 4C020C08 CRC32;

Query Match 18.2%; Score 131; DB 10; Length 509;
Best Local Similarity 31.5%; Pred. No. 0.00017;
Matches 46; Conservative 24; Mismatches 54; Indels 22; Gaps 8;

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QY 7 LVLL----FWIVSGDVMTQSPVLSLPYPGEPAISCRSSQSLAKSYGNTYLSWTL 62
DB 15 LCLLLSASCFCGTGATGTEVKVTOPEKSYVAAGSTILNCVTSLPVG-----PIRW- 70
QY 63 QKPGSPOLLITIGISN--RFSQVDPDRFSGSGSTDTLTKISRVEADVGYVYC-LQ 115
DB 70 RGVGOS-RLIYSFTGEHPRVRNYS--TTRKNMDFSRISNVTPEAGTYVCVKFOR 126
QY 116 GTHOPYT---FGGTKEIKRADAP 138
DB 127 GSSEPDTEIQSGGTEVYVLAKPSPP 152

RESULT 7
ID 031175 PRELIMINARY: PRT: 132 AA.
AC 031175:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MHC CLASS II I-A-ALPHA MRNA (H-2b), 5' END, HYBRIDOMA BBL.D5 PRECURSOR
DE (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 87224052.
RX SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHIKE M.A., TILLINGHAST J.P.,
RA CHOU H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
RA LOH D.Y.;
RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
RT mice.";
RL J. IMMUNOL. 138:3991-3995(1987).
DR EMBL: M16576; G19456; -.
DR PFAM: PF00047; 19; 1.
FT SIGNAL; MHC.
FT NON_TER 1 1
FT SIGNAL <1 19 POTENTIAL.
FT CHAIN 20 >132 POTENTIAL.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14319 MW; 32E47F9C CRC32;

Query Match 18.1%; Score 130; DB 5; Length 132;
Best Local Similarity 31.6%; Pred. No. 5e-05;
Matches 42; Conservative 21; Mismatches 58; Indels 12; Gaps 5;

QY 4 PYRLVLLFWIVSGDVMTQSPVLSLPYPGEPAISCRSSQSLAKSYGNTYLSWTLQ 63
DB 4 PGFVAVILLILRLTRGDSVTOTEGVY--VSEKSLINICTYS--AVSIGPNLFWYR 58
QY 64 KPQSPOLLITVIGISNRFSGVDPDRFSG--SGGTDFTLKISRVEADVGYVYC-LQGH 118
DB 59 YLGEQPOLILKITYTAGQKSSSGFATYKKAETSHLAKASVQESDSAVTYCALNSGT 118
QY 119 QPTFGQGTKEI 131
DB 119 Q--RFGTKILOY 129

RESULT 8
ID 035924 PRELIMINARY: PRT: 509 AA.
AC 035924:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
DE (P84).
GN PTPNS1.
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98012243.
 RA COMO S., WENG W., OLINSKY S., ISHWAD P., MI Z., HEMPEL J., WATKINS S.,
 RA LAGENAUER C.F., NARAYANAN V.,
 RT "The murine p84 neural adhesion molecule is SHPS-1, a member of the
 RT phosphatase-binding protein family.";
 RT J. NEUROSCI. 17:8702-8710(1997).
 DR EMBL: U89694; G2580535; -
 DR MGD; MGI:108563; PTEMSI.
 DR PFAM; PF00047; 19; 3.
 KW SIGNAL.
 FT CHAIN 1 31 POTENTIAL.
 FT CHAIN 32 509 P84.
 SQ SEQUENCE 509 AA; 56056 MW; 3A781050 CRC32;

Query Match 17.9%; Score 129; DB 10; Length 509;
 Best Local Similarity 30.8%; Pred. No. 0.00026;
 Matches 45; Conservative 25; Mismatches 54; Indels 22; Gaps 8;

QY 7 LVLALL----FWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSTYL 62
 DB 15 LCLLLASCFCTGATGKELKVTQPEKSVSAAGDSTVLCNTLTLPLPG----PIKRY- 70
 QY 63 QKPGQSPQLLIYGISN----RFGVDPDRSGSGSTDFTLKISRVEADVGYCL---Q 115
 DB 70 RGVGS-RLLIYSTFGHEPRVRNVSD--TKRNMDSIRISNVTPEAGIYCVKFOR 126
 QY 116 GTHOPYT---FGQTKVEIKRADAP 138
 DB 127 GSSEPDTEIQSGGTEVYVLAKPSP 152

RESULT 9
 Q31174 PRELIMINARY; PRT; 135 AA.
 AC Q31174;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MHC CLASS II I-A-ALPHA MRNA
 DE (H-2B), 5' END, HYBRIDOMA DA.33.C2 PRECURSOR (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87224052.
 RA SPIRELLA D.G., HANSEN T.H., WALSH W.D., BEHLKE M.A., TILLINGHAST J.P.,
 RA CHOI H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
 RA LOH D.Y.,
 RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
 RT mice.";
 RT J. IMMUNOL. 138:3991-3995(1987).
 DR EMBL: M16675; G199454; -
 DR PFAM; PF00047; 19; 1.
 KW SIGNAL; MHC.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 >135 POTENTIAL.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 14646 MW; F60E6A2 CRC32;

Query Match 17.7%; Score 127.5; DB 5; Length 135;
 Best Local Similarity 29.0%; Pred. No. 8.6e-05;
 Matches 40; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

QY 7 LVLALLFWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSTYLAKP 66
 DB 2 LVTVMFLIGRTGDSVI-QMGQVTFSENDSLFINCTYSTT-----GYPLFWYVYISG 60

QY 67 QSPOLLIV-----GISNRFSGVDPFRSGSGTDFTLKISRVEADVGYCL----- 115
 DB 61 EGROLLQVTTANKKSGSRFEATYDK-----GTSEFLHAKTSVQIDSAVYICATSDLS 115
 QY 115 QGTHOPYTFGQTKVEIK 132
 DB 116 GGSNAKLAFGKGTIKLSVK 133

RESULT 10
 088555 PRELIMINARY; PRT; 509 AA.
 AC 088555;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE INHIBITORY RECEPTOR SHPS-1 LONG ISOFORM.
 GN SHPS1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-THYMUS;
 RA VEILLETTE A., THIBAUDEAU E., LATOUR S.,
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RT J. BIOL. CHEM. 0:0-0(1998).
 DR EMBL: AF072543; G3273916; -
 SQ SEQUENCE 509 AA; 55986 MW; 34F9E651 CRC32;

Query Match 16.9%; Score 122; DB 10; Length 509;
 Best Local Similarity 29.3%; Pred. No. 0.0011;
 Matches 43; Conservative 25; Mismatches 55; Indels 24; Gaps 8;

QY 7 LVLALL----FWIPVSGDVMTQSPSLPTPGEPASISCRSSQSLAKSYGNTLYSTYL 62
 DB 15 LCLLLASCFCTGATGKELKVTQPEKSVSAAGDSTVLCNTLTLPLPG----PIKRY- 70
 QY 63 QKPGQSPQLLIYGISN----RFGVDPDRSGSGSTDFTLKISRVEADVGYCL--- 115
 DB 70 --RGVGSRLIYSTFGHEPRVRNVSD--TKRNMDSIRISNVTPEAGIYCVKFO 125
 QY 115 QGTHOPYT---FGQTKVEIKRADAP 138
 DB 126 GSSEPDTEIQSGGTEVYVLAKPSP 152

RESULT 11
 088555 PRELIMINARY; PRT; 291 AA.
 AC 088555;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE INHIBITORY RECEPTOR SHPS-1 SHORT ISOFORM.
 GN SHPS1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-THYMUS;
 RA VEILLETTE A., THIBAUDEAU E., LATOUR S.,
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RT J. BIOL. CHEM. 0:0-0(1998).
 DR EMBL: AF072544; G3273918; -
 SQ SEQUENCE 291 AA; 31735 MW; C892D685 CRC32;

Query Match 16.7%; Score 120; DB 10; Length 291;
 Best Local Similarity 30.0%; Pred. No. 0.00094;
 Matches 42; Conservative 24; Mismatches 50; Indels 24; Gaps 8;

QY 7 LVLLVLT-----FWIPVSGDVMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWY 62
 DB 15 LVCILLSASCFCTGATCKELKATVOPKSVSAAGDSTVLTCTLTSLPVG---PIRWY- 70
 QY 63 QKPGQSP-QLLIYGISN-----RFGVDPDRFSGSGSDTFLTKISRYEADVGYYCYL- 115
 DB 70 --RGVGSRLIISFAEYYPRIHNVSD--TTRKNNMDFSRISNVPADAGIYCYKFG 125
 QY 115 QGTHQPYT---FPGGKVEI 131
 DB 126 KGSSEPTDEIOSGGTGYV 145

RESULT 12
 ID 016237 PRELIMINARY; PRT; 145 AA.
 AC 016237;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE VPRE-B. PROTEIN.
 GN VPRE-B.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 95021318.
 RA GUELA-FONLUP V., BOSSY D., ALZARI P., FUMOUX F., FOUGEREAU M.,
 RA SCHIFF C.;
 RT "The human pre-B cell receptor: structural constraints for a tentative
 RT model of the pseudo-light (psi L) chain."
 RL MOL. IMMUNOL. 31:1099-1108(1994).
 DR EMBL; S74019; 6693811; -
 DR PRAW; PF00047; 19; 1.
 SQ SEQUENCE 145 AA; 16605 MW; 7E7002CB CRC32;

Query Match 15.9%; Score 114.5; DB 2; Length 145;
 Best Local Similarity 30.0%; Pred. No. 0.0014;
 Matches 36; Conservative 21; Mismatches 44; Indels 19; Gaps 7;

QY 9 VLLFWIPVSG-GDVMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWYLOKP 65
 DB 6 VLLMFLFYCTGCGPQPLHQPAMSSALGTTIRLTCTLRNDHDI---GYSVYMYOQRP 61
 QY 66 GSPOLLIT--YGISNRFSG--VPDRFSGSGSGTDF-----LKISRYEADVGYYCYLOG 116
 DB 62 GHPRFLRFRFSQSDKSGQGVPPRFSGS---KDYARNRGLTSLSELOPEDENYTCAMG 118

RESULT 13
 ID 070153 PRELIMINARY; PRT; 228 AA.
 AC 070153;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE B29/TG-BETA/CD79B.
 GN B29/TG-BETA.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIDROGNATHI; MORIDAE; MORINAE; RATTUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE; 98207252.
 RA NAKAZATO S., NOMOTO K., KAZAHARI K., ONO M.;
 RT "Physical linkage of the B29/Ig-beta (CD79b) gene to the skeletal

RT muscle, sodium-channel, and growth hormone genes in rat and human";
 RL GENOMICS 48:363-368(1998).
 DR EMBL; AB004831; D1026583; -
 SQ SEQUENCE 228 AA; 25865 MW; 03F8D7C6 CRC32;

Query Match 15.9%; Score 114.5; DB 10; Length 228;
 Best Local Similarity 28.3%; Pred. No. 0.0023;
 Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 7;

QY 8 LVLLFWIPVSGDVMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWY 57
 DB 17 LLLLLSGEVPV---AWTKSD-QPPIFGSPCSKIQHPFAAKRSSMWKFFCHDYSG 71
 QY 57 YLSWYLOKPGQSPOLLITYGISNRFSGVDP--RFGSGSGSDTFLTKISRYEADVGYYCYL 114
 DB 72 VMTWFRKGNQROLEF-----PEDGHISQTFNGSVYTLTNTQYEDNGITFCQ 121
 QY 115 Q---GTHQPYTFGGKTV 129
 DB 122 QKCNSTEPDVTDCGTGL 139

RESULT 14
 ID 031177 PRELIMINARY; PRT; 132 AA.
 AC 031177;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE MHC CLASS II I-A-ALPHA MRNA
 DE (H-2B), 5' END, HYBRIDOMA AF.3.G7 PRECURSOR (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIDROGNATHI; MORIDAE; MORINAE; MUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 87224052.
 RA SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHRE M.A., TILLINGHAST J.P.,
 RA CHOU H.S., WHITELEY P.J., KARP J.A., PIERCE C.W., SHEVACH E.M.,
 RA LOH D.Y.;
 RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
 RT mice."
 RL J. IMMUNOL. 138:3991-3995(1987).
 DR EMBL; M16678; G199460; -
 DR PRAW; PF00047; 19; 1.
 KW SIGNAL; MHC.
 FT SIGNAL. 1 19
 FT CHAIN 20 >132 POTENTIAL.
 FT NON_TER 132 132
 SQ SEQUENCE 132 AA; 14674 MW; 9364DDAD CRC32;

Query Match 15.6%; Score 112.5; DB 5; Length 132;
 Best Local Similarity 30.7%; Pred. No. 0.002;
 Matches 42; Conservative 16; Mismatches 58; Indels 21; Gaps 6;

QY 7 LVLLVLT-----FWIPVSGDVMTQSPSLPYTPGEPASISCRSSQSLAKSYGNTYLSWY 61
 DB 2 LVVLSIFLGIFHFLDVTQTV--SQSDAHYTFEGDSVELEKRYSYG-----GSITYSWY 54
 QY 62 LKPGQSPOLLITYGISNR-----FSGVDPDRFSGSGSDTFLTKISRYEADVGYYCYLOG 116
 DB 55 IOHHGHLQFLKRYSGNPVYGVNGEAEAFSSDS--STHLKASVHMSDAVYFCAYR 112
 QY 117 THQ--PYTFGGKVEI 131
 DB 113 TASLGKLFQGTQGVV 129

RESULT 15
 ID 031176 PRELIMINARY; PRT; 118 AA.

AC 031176;
 DT 01-NOV-1996 (TREMBLER, 01, CREATED)
 DT 01-NOV-1996 (TREMBLER, 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLER, 08, LAST ANNOTATION UPDATE)
 DE MHC CLASS II T-A-ALPHA mRNA (H-2B), 5' END, HYBRIDOMA Z238 PRECURSOR
 DE (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87224052.
 RA SPINELLA D.G., HANSEN T.H., WALSH W.D., BEHRE M.A., TILLINGHAST J.P.,
 RA CHOU H.S., WHITELEY P.J., KAPP J.A., PIERCE C.W., SHEVACH E.M.,
 RA LOH D.Y.;
 RT "Receptor diversity of insulin-specific T cell lines from C57BL (H-2b)
 mice";
 RL J. IMMUNOL. 138:3991-3995(1987).
 DR EMBL: M16677; G199458; .
 DR PFAM: PF00047; 1g; 1.
 KW SIGNAL; MHC.
 FT NON_TER 1 1
 FT SIGNAL <1 5 POTENTIAL.
 FT CHAIN 6 >118 POTENTIAL.
 FT NON_TER 118 118
 SQ SEQUENCE 118 AA; 13271 MW; 9447ADEE CRC32;

Query Match 15.58; Score 111.5; DB 5; Length 118;
 Best Local Similarity 28.28; Pred. No. 0.0021;
 Matches 35; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

OY 18 SGGDVWVTOSPLSLPVTGEPASISCRSSQSLAKSYGNTYLSYLOKPGOSPOLLTYGIS 77
 DB 3 SNEDSV-TQTEGLVYTEGLPVLNLC-----TYQTAISDVAFETVYQHLNAPKLL----- 54
 OY 78 NRESGVDPDRFSGSG-----SGTDFTLKISRVEADVGYYCL--QGT HQPYTFGQGR 128
 DB 54 -RSTDNKRTRHQGFHATLHKSSSPFLQKSSVQLSDSALYFCALSRNNNNRIFFGDGTQ 112
 OY 129 VEIK 132
 DB 113 LVVK 116

Search completed: May 11, 1999, 12:21:02
 Job time: 254 sec

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OM protein - protein search, using sw model

Run on: May 11, 1999, 12:14:57 ; Search time 44.09 Seconds
(without alignments)
63.304 Million cell updates/sec

Title: US-08-700-737-21

Perfect score: 720
Sequence: 1 MKLPVRLVLLFWIPVSGG.....QPTFGGQTKVEIKRADAP 138

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database: A_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	712	98.9	138	1 W53812	Light chain of a h
2	646	89.7	140	1 W53817	Consensus protein
3	616	85.6	132	1 W53814	Murine Act-1 light
4	582.5	80.9	131	1 R52822	Humanised murine K
5	582.5	80.9	131	1 R70470	Humanised anti-KC-
6	582.5	80.9	131	1 W03199	Anti-Idiotypic mono
7	579	80.4	139	1 W71876	Anti-human Fas hum
8	579	80.4	139	1 W71877	Anti-human Fas hum
9	575	79.9	239	1 W18777	Anti-human Fas hum
10	575	79.9	239	1 W18779	Anti-human Fas hum
11	574.5	79.8	238	1 W14942	3F4 Human IgG4 exp
12	574.5	79.8	238	1 W14937	Murine anti-porcine
13	570.5	79.2	131	1 W34518	Variable kappa cha
14	570.5	79.2	238	1 W31572	L chain subunit of
15	570.5	79.2	238	1 W1889	Anti-human Fas mon
16	564.5	78.4	131	1 R52806	Humanised murine B
17	562.5	78.1	172	1 R15199	Variable light cha
18	561.5	78.0	140	1 W68492	Variable light cha
19	558	77.5	150	1 R1598	Murine monoclonal
20	549.5	76.3	131	1 R32241	Chimeric MAb light
21	549.5	76.3	131	1 R31887	BR55-2 light chain
22	545.5	75.8	131	1 R52772	Murine KC-4 immuno
23	545.5	75.8	131	1 R52790	Murine KC-4 immuno
24	545.5	75.8	131	1 R70457	Variable region of ant
25	545.5	75.8	132	1 W60867	BR55-2 murine IgG3
26	543.5	75.5	131	1 R32245	Murine anti-ICAM m
27	538.5	74.8	173	1 R15059	Sequence of the VL
28	536	74.4	135	1 R54052	Monoclonal antibody
29	536	74.4	135	1 W01525	Monoclonal antibody
30	536	74.4	135	1 W24989	Monoclonal antibody
31	535	74.3	239	1 W01819	Primitised anti-hu
32	535	74.3	239	1 W63762	Macaque primatized
33	535	74.3	139	1 W1887	Anti-Fas MAb CH11
34	532.5	74.0	238	1 R93554	Monoclonal antibody
35	530	73.6	116	1 W76126	Human ICR-8.1 V-K
36	530	73.6	116	1 W71256	Humanised murine a
37	528.5	73.4	131	1 R09424	Co-1 light chain V
38	528.5	73.4	131	1 W06214	Mab Co-1 light cha
39	522	72.5	112	1 R32239	Humanised MAb ligh
40	522	72.5	112	1 W27145	Mature light chain
41	522	72.5	112	1 W54015	Human Anti-CD4 ant
42	517.5	71.9	131	1 R52788	Murine BRE-3 immu
43	517.5	71.9	131	1 R52770	Murine BRE-3 immu

ALIGNMENTS

RESULT ID	1	W53812	W53812 standard; Protein; 138 AA.	44	514	71.4	132	1	W50219	Amino acid sequenc
AC	W53812	W53812	W53812	45	511	71.0	112	1	R95212	HumB3V1 humanised
DE	14-JUL-1998 (first entry)									
KW	Light chain of a humanised murine Act-1 antibody.									
KW	Mouse; Act-1 antibody; human alpha4-beta7 integrin;									
KW	Muscosal adressin cell adhesion molecule-1; MacCAM-1;									
KW	humanised antibody; murine antigen binding region; inhibition;									
KW	leukocyte infiltration of tissue; treatment; inflammatory disease;									
KW	inflammatory bowel disease.									
OS	Synthetic.									
OS	Mus sp.									
OS	Homo sapiens.									
FH	Key	Location/Qualifiers								
FT	Peptide	1..20 "signal peptide"								
FT	Protein	21..138								
FT		/note="mature protein"								
PN	W09806248-A2.									
PD	19-FEB-1998.									
PF	06-AUG-1997; U13884.									
PR	15-AUG-1996; US-700737.									
PA	(LEUK-) LEUKOSITE INC.									
PI	Bending MM, Jones ST, Newman W, Ponath PD, Ringler DJ, Saldanha J;									
DR	WPI: 98-159172/14.									
DR	N-PSDB; V20075.									
PT	Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -									
PT	used for treating inflammatory disease, pancreatitis, diabetes,									
PT	asthma, graft versus host disease and sarcoidosis									
PS	Claim 15; Fig 12; 145pp; English.									
CC	The present sequence represents the light chain of humanised murine									
CC	antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.									
CC	Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of									
CC	this particular integrin. The Act-1 antibody interferes with alpha4-beta7									
CC	integrin binding to MacCAM-1, which is present of high endothelial									
CC	venules in mucosal lymph nodes. The humanised immunoglobulin can be									
CC	used to inhibit the interaction of cells bearing alpha4-beta7 with									
CC	cells bearing a ligand for alpha4-beta7. It can be used for inhibiting									
CC	leukocyte infiltration of tissues, e.g. for treating inflammatory									
CC	diseases such as inflammatory bowel disease. The immunoglobulin can									
CC	also be used for detection, isolation and diagnosis.									
SQ	Sequence 138 AA:									

Query Match 98.9%; Score 712; DB 1; Length 138;
Best Local Similarity 99.3%; Pred. No. 1.1e-45;
Matches 137; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKLPVRLVLLFWIPVSGGDDVVTQSPFLPTPGGPASISCRSSQSLAKSGNTYLSW	60
DB	1	MKLPVRLVLLFWIPVSGGDDVVTQSPFLPTPGGPASISCRSSQSLAKSGNTYLSW	60
QY	61	YLOKPGSPOLLTYGISNRPSSGVDPDRPSSGSGNDFTLKISRYEADGVYCYLOGTHOP	120
DB	61	YLOKPGSPOLLTYGISNRPSSGVDPDRPSSGSGNDFTLKISRYEADGVYCYLOGTHOP	120
QY	121	YTFGGQTKVEIKRADAP 138	
DB	121	YTFGGQTKVEIKRADAP 138	
RESULT ID	2	W53817	
		W53817 standard; Protein; 140 AA.	

AC W53814; (first entry)
 DT 14-JUL-1998
 DE Consensus protein sequence of the murine variable light chain region.
 KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease.
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT /note- "signal peptide"
 FT /note- "mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PE 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 PI WPI: 98-159172/14.
 DR N-PSDB: V20086.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Example 1; Fig 3; 145pp; English.
 CC The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse light chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in muscosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 SQ Sequence 140 AA;

Query Match 89.7%; Score 646; DB 1; Length 140;
 Best Local Similarity 88.4%; Pred. No. 7.5e-41;
 Matches 122; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGDVYVNTQSPSLPTPFGEPASISCRSSSGLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGDVYVNTQSPSLPTPFGEPASISCRSSSGLAKSYGNTYLSW 60
 QY YLQKPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 DB 61 YLHAFPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 QY 121 YTFGGGTKEIKRADAP 138
 DB 121 YTFGGGTKEIKRADAP 138

RESULT 3
 W53814
 ID W53814 standard; Protein; 132 AA.
 AC W53814;
 DT 14-JUL-1998 (first entry)
 DE Murine Act-1 light chain variable region.
 KM Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KM Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KM inflammatory bowel disease.

KM humanised antibody; murine antigen binding region; inhibition;
 KM leukocyte infiltration of tissue; treatment; inflammatory disease;
 KM inflammatory bowel disease.
 OS Mus sp.
 FH Key
 FT Peptide
 FT Protein
 FT /note- "signal peptide"
 FT /note- "mature protein"
 PN W09806248-A2.
 PD 19-FEB-1998.
 PE 06-AUG-1997; U13884.
 PR 15-AUG-1996; US-700737.
 PA (LEUK-) LEUKOSITE INC.
 PI Bendig KM, Jones ST, Newman W, Ponath PD, Ringler DJ,
 PI Saldanha J;
 PI WPI: 98-159172/14.
 DR N-PSDB: V20077.
 PT Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 PS Claim 23; Fig 7; 145pp; English.
 CC The present sequence represents the light chain variable region of
 CC murine antibody Act-1. Act-1 is active against human alpha4-beta7
 CC integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a
 CC ligand of this particular integrin. The Act-1 antibody interferes with
 CC alpha4-beta7 integrin binding to MadCAM-1, which is present of high
 CC endothelial venules in muscosal lymph nodes. Humanised Act-1 can be used
 CC to inhibit the interaction of cells bearing alpha4-beta7 with cells
 CC bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 SQ Sequence 132 AA;

Query Match 85.6%; Score 616; DB 1; Length 132;
 Best Local Similarity 87.9%; Pred. No. 1.1e-38;
 Matches 116; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGGDVYVNTQSPSLPTPFGEPASISCRSSSGLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFWIPVSGGDVYVNTQSPSLPTPFGEPASISCRSSSGLAKSYGNTYLSW 60
 QY YLQKPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 DB 61 YLHAFPGSPOLLITIGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYICLQGTROP 120
 QY 121 YTFGGGTKEIKRADAP 132
 DB 121 YTFGGGTKEIKRADAP 132

RESULT 4
 R52822
 ID R52822 standard; Protein; 131 AA.
 AC R52822;
 DT 25-JAN-1995 (first entry)
 DE Humanised murine KC-4 immunoglobulin light chain V-region.
 KM Immunoglobulin variable domain; primer; polymerase chain reaction;
 KM chimeric antibody; human mammary fat globule; human breast carcinoma;
 KM murine anti-HMFG monoclonal antibody KC-4; humanised analogue.
 OS Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 PN W09411509-A.
 PD 26-MAY-1994.
 PE 16-NOV-1993; U11445.
 PR 16-NOV-1992; US-977696.
 PR 30-SEP-1993; US-129930.
 PR 08-OCT-1993; US-134346.
 PA (CANC-) CANCER RES FUND CONTRA COSTA.
 PI Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
 DR WPI: 94-183510/22.

DR N-PSDB: 062803.
 PT New analogue peptide(s) comprising antibody variable regions -
 PT used to develop prods. for use in the detection, diagnosis,
 PT therapy and prevention of neoplasms.
 PS Example 75: Page 95: 109pp: English.
 CC This sequence represents a humanised murine anti-human carcinoma
 CC KC-4 antibody light chain variable region. The humanised antibody is
 CC useful for carcinoma therapy and diagnosis and for in vivo imaging
 CC of neoplastic cells. It is also of use in inhibiting the growth of
 CC a primary or metastasised neoplasm.
 SQ Sequence 131 AA;

Query Match 80.9%; Score 582.5; DB 1; Length 131;
 Best Local Similarity 84.1%; Pred. No. 3e-36;
 Matches 11; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSQSIASGYNTYLSW 60
 DB 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSQSIASGYNTYLSW 59

QY YLQKPGSPOLLITKYSIRFSGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 120
 DB YLQKPGSPOLLITKYSIRFSGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 119

QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 5
 R70470
 ID R70470 standard; Protein; 131 AA.

AC R70470;
 DT 27-OCT-1995 (first entry)
 DE Humanised anti-KC-4 antibody VL FR-HZ.
 KW Anti-KC-4 antibody; humanised antibody; cancer.
 OS Synthetic.
 PN WO9510776-A.
 PD 20-APR-1995.
 PF 16-NOV-1993; U11444.
 PR 08-OCT-1993; US-134346.
 PA (CANC.) CANCER RESEARCH FUND CONTRA COSTA.
 PI Certani RL, Docouto JFR, Peterson JA;
 DR WPI: 95-161912/21.
 DR N-PSDB: 087533.

PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells. In vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PS Claim 2: Table 24, Page 51; 61pp: English.
 CC Hybridomas were prep. based on the anti-KC-4 mouse hybridoma ATCC
 CC HB 8710 (US4708930). The murine variable regions were modified at
 CC particular AAs by PCR to provide humanised sequences. The anti-KC-4
 CC humanised DNA sequences for the VH and VL segments are shown in
 CC Q87534 and Q87533 respectively. Plasmid constructions comprising
 CC the humanised variable regions and the human constant regions were
 CC then used to transfect SP2/0-Ag14 myeloma cells to produce the
 CC humanised anti-KC-4 mAbs. The deduced AA sequences of the
 CC humanised anti-KC-4 variable light and heavy chains are given in
 CC R70470 and R70471 respectively.
 SQ Sequence 131 AA;

Query Match 80.9%; Score 582.5; DB 1; Length 131;
 Best Local Similarity 84.1%; Pred. No. 3e-36;
 Matches 11; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSQSIASGYNTYLSW 60
 DB 1 MKLPLVRLVLLFMFIPVSGGVMTQSLPVPPEPASISCRSSQSIASGYNTYLSW 59

QY YLQKPGSPOLLITKYSIRFSGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 120
 DB YLQKPGSPOLLITKYSIRFSGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 119

DB 60 YLQKPGSPOLLITKYSIRFSGVDPDRFSGSGGTDFTLKISRVEAEDVGYTCFQGSHP 119
 QY 121 YTFGGGTRLEIK 132
 DB 120 YTFGGGTRLEIK 131

RESULT 6
 W03199
 ID W03199 standard; Protein; 149 AA.

AC W03199;
 DT 26-FEB-1997 (first entry)
 DE Anti-Idiotypic monoclonal antibody 1A7 variable light chain.
 KW Murine; mouse; anti-Idiotypic; monoclonal antibody; Mab; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 OS Mus musculus.

FT Key location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT region 20..42
 FT /note="framework region 1"
 FT 43..58
 FT /note="complementarity determining region 1"
 FT 59..73
 FT /note="framework region 2"
 FT 74..80
 FT /note="complementarity determining region 2"
 FT 81..112
 FT /note="framework region 3"
 FT 113..121
 FT /note="complementarity determining region 3"
 FT 122..131
 FT /note="framework region 4"

PN WO9622373-A2.
 PD 25-JUL-1996.
 PF 17-JAN-1996; U00882.
 PR 17-JAN-1995; US-372676.
 PR 16-JAN-1996; US-372676.
 PA (KENT) UNIV KENTUCKY.
 PI Chatterjee M, Chatterjee SK, Foon KA;
 DR WPI: 96-354530/35.
 DR N-PSDB: T31332.

PT Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 PS Claim 8: Fig 1: 14pp: English.

CC The present sequence is that of the murine anti-Idiotypic monoclonal
 CC antibody (Mab) 1A7 variable light chain. Mab 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) Mab 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, Mab 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.

CC Mab 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and
 CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.

CC The cDNA can be used in expression systems for 1A7 prod., and in
 CC the prep. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 SQ Sequence 149 AA;

sequence (see V61359), and host cells such as *Escherichia coli*

CC expressing Fas (e.g. synovialocytes) and are useful in the treatment

CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are
 CC vectors such as pKappakF2-10 including the VL-RF nucleotide
 CC sequence (see V61361), and host cells such as Escherichia coli
 CC pKappakF2-10 (FERM BP-5859).
 SO Sequence 239 AA;

Query Match 80.4%; Score 579; DB 1; Length 239;
 Best Local Similarity 81.2%; Pred. No. 9,8e-36;
 Matches 112; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKLPRLVLLFMTPVSGGVMTQSPSLPVPPEPASISCRSSQSIASVNTYISM 60
 Db 1 MRLPQLGLMLMWPGSSGVMTQSPSLPVLIGOPASISCRSSKSLVHSGNTYILW 60
 QY 61 YLQKPGSPQLLIYGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYCLOGTHP 120
 Db 61 YLQKPGSPRLTIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYCLOGTHP 120
 QY 121 YTFGGTKEIKRADAP 138
 Db 121 PAFGGTKEIKRTVAAP 138

RESULT 9
 W71877
 ID W71877 standard; Protein; 239 AA.

AC W71877;
 DT 18-JAN-1999 (first entry)
 DE Anti-human Fas humanised antibody CH11 light chain VL-RF.
 KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT 21..239
 FT Region /label= Mat_protein
 FT 44..59
 FT /label= CDR1
 FT /note= "complementarity determining region 1 from
 Region CH11 light chain"
 FT 75..81
 FT /label= CDR2
 FT /note= "complementarity determining region 2 from
 Region 114..122
 FT /label= CDR3
 FT /note= "complementarity determining region 3 from
 CH11 light chain"

PN EP-866131-A2.
 PD 23-SEP-1998.
 PE 20-MAR-1998; 302113.
 PR 21-MAR-1997; JP-067938.
 PA (SANY) SANKYO CO LTD.
 PI Haruyama H, Nakahara K, Serizawa N, Takahashi T,
 PI Yonehara S;
 DR WPI; 98-482965/42.
 DR N-PSDB; V61360.
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Claim 23; Page 96-97; 187pp; English.
 CC This is the amino acid sequence of a humanised anti-Fas antibody
 CC CH11 light chain, designated VL-RF. VL-RF is based on the light
 CC chain (see W71889) of murine anti-human Fas monoclonal antibody
 CC CH11. The humanised sequence was designed following selection of
 CC donor residues from CH11 to be grafted onto acceptor molecule
 CC RPA1610/CL. 4 light chain sequences (see W71876-79) have been
 CC designed, and each can be used in combination with either of 2

CC heavy chain sequences (see W71880-81) to provide novel, claimed
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells
 CC expressing Fas (e.g. synovocytes) and are useful in the treatment
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are
 CC vectors such as pKappakF2-19 including the VL-RF nucleotide
 CC sequence (see V61360), and host cells such as Escherichia coli
 CC pKappakF2-19 (FERM BP-5860).
 SO Sequence 239 AA;

Query Match 79.9%; Score 575; DB 1; Length 239;
 Best Local Similarity 80.4%; Pred. No. 1,3e-35;
 Matches 111; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 MKLPRLVLLFMTPVSGGVMTQSPSLPVPPEPASISCRSSQSIASVNTYISM 60
 Db 1 MRLPQLGLMLMWPGSSGVMTQSPSLPVLIGOPASISCRSSKSLVHSGNTYILW 60
 QY 61 YLQKPGSPQLLIYGISNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYCLOGTHP 120
 Db 61 YLQKPGSPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVAEDVGYVYCLOGTHP 120
 QY 121 YTFGGTKEIKRADAP 138
 Db 121 PAFGGTKEIKRTVAAP 138

RESULT 10
 W71879
 ID W71879 standard; Protein; 239 AA.

AC W71879;
 DT 18-JAN-1999 (first entry)
 DE Anti-human Fas humanised antibody CH11 light chain VL-RF.
 KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT 21..239
 FT Region /label= Mat_protein
 FT 44..59
 FT /label= CDR1
 FT /note= "complementarity determining region 1 from
 Region CH11 light chain"
 FT 75..81
 FT /label= CDR2
 FT /note= "complementarity determining region 2 from
 Region 114..122
 FT /label= CDR3
 FT /note= "complementarity determining region 3 from
 CH11 light chain"

PN EP-866131-A2.
 PD 23-SEP-1998.
 PE 20-MAR-1998; 302113.
 PR 21-MAR-1997; JP-067938.
 PA (SANY) SANKYO CO LTD.
 PI Haruyama H, Nakahara K, Serizawa N, Takahashi T,
 PI Yonehara S;
 DR WPI; 98-482965/42.
 DR N-PSDB; V61362.
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Claim 27; Page 101-102; 187pp; English.
 CC This is the amino acid sequence of a humanised anti-Fas antibody
 CC CH11 light chain, designated VL-RF. VL-RF is based on the light
 CC chain (see W71889) of murine anti-human Fas monoclonal antibody

CC CH11. The humanised sequence was designed following selection of
 CC donor residues from CH11 to be grafted onto acceptor molecule
 CC RPM6410/C1. 4 light chain sequences (see W1876-79) have been
 CC designed, and each can be used in combination with either of 2
 CC heavy chain sequences (see W1880-81) to provide novel, claimed
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells
 CC expressing Fas (e.g. synovocytes) and are useful in the treatment
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised rheumatoid arthritis, as are
 CC vectors such as pKappaRF2-52 including the VL-RF nucleotide
 CC sequence (see V61362), and host cells such as Escherichia coli
 CC pKappaRF2-52 (FERM BP-5862).
 SQ Sequence 239 AA;

Query Match 79.8%; Score 575; DB 1; Length 239;
 Best Local Similarity 80.4%; Pred. No. 1.9e-35;
 Matches 11; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 OY 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 OY 121 YTFGGGTKEIKRADAAP 138
 121 YTFGGGTKEIKRADAAP 138
 DB 121 YTFGGGTKEIKRADAAP 138
 121 YTFGGGTKEIKRADAAP 138

RESULT 11

W14942
 ID W14942 standard; Protein: 238 AA.

AC W14942:
 DT 16-JUN-1997 (first entry)
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 PN M09711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR N-PSDB: T62938.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure; Page 65-66; 105pp; English.
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W1937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 SQ Sequence 238 AA;

Query Match 79.8%; Score 574.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 2.1e-35;
 Matches 11; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 OY 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 OY 121 YTFGGGTKEIKRADAAP 138
 121 YTFGGGTKEIKRADAAP 138
 DB 121 YTFGGGTKEIKRADAAP 138
 121 YTFGGGTKEIKRADAAP 138

RESULT 12

W14937
 ID W14937 standard; Protein: 238 AA.

AC W14937:
 DT 16-JUN-1997 (first entry)
 DE Murine anti-porcine VCAM 3F4 light chain.
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KM vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KM chimeric antibody; diagnosis.
 OS Mus sp.
 FH Key
 FT region Location/Qualifiers
 FT region 43..58
 FT region /label= CDR1
 FT region 74..80
 FT region /label= CDR2
 FT region 113..121
 FT region /label= CDR3
 PN M09711971-A1.
 PD 03-APR-1997.
 PF 27-SEP-1996; U15575.
 PR 28-SEP-1995; US-004489.
 PR 26-SEP-1996; US-004489.
 PA (ALEX-) ALEXION PHARM INC.
 PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 DR N-PSDB: T62934.
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 PS Disclosure; Page 52-53; 105pp; English.
 CC Light chain (W14937) and heavy chain (W14938) sequences are
 CC provided for the murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody (MAb) 3F4. Hybridoma 3F4 was
 CC produced by standard techniques using recombinant, soluble porcine
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
 CC MAb 3F4 and 2A2 (see also W14931-32) variable regions into
 CC expression plasmid pAPEX-3P modified to contain the human gamma4
 CC constant region in place of the human gamma1 region. Sequences
 CC are provided for 3F4 (chimeric) human G2/G4 cDNA (W14939), a 3F4
 CC human G2/G4 expression plasmid insert product (W14940), and 3F4
 CC human IgG4 expression plasmid insert products (W14941-42). The
 CC chimeric antibodies are specific for porcine VCAM. They are useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 SQ Sequence 238 AA;

Query Match 79.8%; Score 574.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 2.1e-35;
 Matches 11; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

OY 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMWIPVSGDVMTQSPSLPVTPEEPASISCRSSQSLAKSYGNTYLSW 60
 OY 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 DB 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120
 61 YLQKPGQSPOLLITIGISNRRSGVDPDRFSGSGSTDTLKISRVEADGVYVYCCLOGTHP 120

QY 121 YTFGGGKVEIKRADAP 138
 DB 120 FTFGGGKLEIKRTVAAP 137

RESULT 13

W34518
 ID W34518 standard; Protein; 131 AA.
 AC W34518;
 DT 19-MAR-1998 (first entry)
 DE Variable kappa chain of antibody from hybridoma 1-706-139.
 KW Variable region coding sequence; constant region epitope; hybridoma;
 KW antibody detection; antigen/antibody complex; variable heavy chain.
 OS Mus musculus.
 PN WO9272486-A1.
 PD 31-JUL-1997.
 PF 17-JAN-1997; UO1074.
 PR 23-JAN-1996; US-589939.
 PA (ABBO) ABBOTT LAB.
 PI Golden AM, Hackett JR, Hoff JA, Ostrow DH;
 DR WPI: 97-393833/36.
 DR N-PSDB: T98835.
 PT Use of antibody constant region epitope(s) - as control or
 PT calibrator reagents in assays for detecting the presence of an
 PT antibody in a test sample
 PS Disclosure; Page 62-63; 109pp; English.
 CC This sequence represents the variable kappa chain of the antibody
 CC produced by hybridoma 1-706-139, and can be detected using the method of
 CC the invention. The method is for detecting the presence of antibody which
 CC may be present in a test sample. It comprises contacting a test sample
 CC suspected of containing the antibody with an antigen specific for the
 CC antibody to allow the formation of antigen/antibody complexes, detecting
 CC the presence of the antibody which may be present in the test sample and
 CC employing, as a control or calibrator a reagent which binds to the
 CC antigen. The improvement to this method over previous methods, comprises
 CC employing, as the control or calibrator, a reagent comprising one or more
 CC antibody constant region epitopes, where the reagent binds to the antigen
 CC and is homogeneous with respect to specificity and affinity. The method
 CC can also be used for detecting the presence of antibodies developed
 CC against more than one antigen. The method is used particularly for the
 CC detection of human antibodies specific for a given antigen, e.g. HIV-1,
 CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all
 CC of the problems associated with using an immune sera in the manufacture
 CC of calibrators and positive controls. The present reagents can be readily
 CC and reproducibly generated in virtually unlimited quantities and are also
 CC useful for quantitating, and monitoring the integrity of, the antigen
 CC used in assays.
 SQ Sequence 131 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 131;

Best Local Similarity 82.6%; Pred. No. 2.3e-35;

Matches 109; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFMIPYSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMIPYSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 59
 QY 61 YLQKPGSPOLLIVGISNRSFSGVDPDRFSGSGGTDFLTKISRVAEDVGYTCLOGTHOP 120
 DB 60 YLQKPGSPOLLIVKYSNRSFSGVDPDRFSGSGGTDFLTKISRVAEDLVGYFCQSQSTHPV 119
 QY 121 YTFGGGKVEIK 132
 DB 120 WTFGGGKLEIK 131

RESULT 14

W31752
 ID W31752 standard; Protein; 238 AA.
 AC W31752;
 DT 15-APR-1998 (first entry)

DE L chain subunit of Fas specific antibody.
 KW Fas; antibody; human; immunoglobulin; variable region; rheumatism;
 KW autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain;
 KW complementarity determining region.
 OS Mus musculus.

FN Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note="signal peptide"

FT /note="mature protein"

PN EP-799891-A1.

PD 08-OCT-1997.

PF 27-MAR-1997; 302415.

PR 01-APR-1996; JP-078570.

PA (SANY) SANKYO CO LTD.

PI Ichikawa K, Nakahara K, Serizawa N, Yonehara S;
 DR WPI: 97-482673/45.

DR N-PSDB: T88870.

PT Anti-Fas recombinant antibodies - useful for treating auto-immune
 PT diseases, especially rheumatoid arthritis

PS Claim 12; Page 34-35; 72pp; English.

CC This sequence represents the light chain of the protein of the invention.
 CC The protein of the invention is a recombinant protein (A), that comprises
 CC at least one region corresponding to an immunoglobulin (Ig) variable
 CC region which enables the protein to recognise and specifically bind to an
 CC antigen, preferably human Fas, and has substantially no more
 CC immunogenicity in a human patient than a human antibody. The proteins are
 CC useful for treating autoimmune diseases, especially rheumatism
 CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As
 CC the protein lacks the constant region, it has substantially no more
 CC immunogenicity in the human patient than a human antibody.

SQ Sequence 238 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 238;

Best Local Similarity 81.2%; Pred. No. 4.1e-35;

Matches 112; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFMIPYSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 60
 DB 1 MKLPVRLVLLFMIPYSGDVVMTQSPSLPYTPGPASISCRSSOSLAKSYGNTYLSW 59
 QY 61 YLQKPGSPOLLIVGISNRSFSGVDPDRFSGSGGTDFLTKISRVAEDVGYTCLOGTHOP 120
 DB 60 YLQKPGSPOLLIVKYSNRSFSGVDPDRFSGSGGTDFLTKISRVAEDLVGYFCQSQSTHPV 119
 QY 121 YTFGGGKVEIKRADAP 138
 DB 120 PAFGGGKLEIKRADAP 137

RESULT 15

W71889
 ID W71889 standard; Protein; 238 AA.

AC W71889;
 DT 18-JAN-1999 (first entry)

DE Anti-human Fas monoclonal antibody CH11 light chain.
 KW Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
 KW antibody engineering.

OS Mus musculus.

FN Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Sig_peptide

FT /label= Mat_protein

FT Region 43..58

FT /label= CDR1

FT Region 74..80

FT /label= CDR2

FT 113..121

FT /label= CDR3

PN EP-866131-A2;
 PD 23-SEP-1998;
 PF 20-MAR-1998; 302113.
 PR 21-MAR-1997; JP-067938.
 PA (SANY) SANKYO CO LTD.
 PI Haruyama H, Nakahara K, Serizawa N, Takahashi T,
 PI Yonehara S;
 DR WPI; 98-482965/42.
 DR N-PSDB; V66736.
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Reference Example 4; Page 62-63; 187pp; English.
 CC This is the amino acid sequence of the light chain of the
 CC mouse anti-human Fas monoclonal antibody CH1, as deduced from an
 CC amplified cDNA clone (see V66736). The invention relates to novel
 CC humanised antibodies comprising humanised light and heavy chains
 CC (see W71876-81) of CH1. These humanised anti-human Fas antibodies
 CC are capable of inducing apoptosis in cells expressing Fas (e.g.
 CC synovialocytes) and are useful in the treatment of autoimmune disease
 CC and chronic rheumatoid arthritis.
 SQ Sequence 238 AA;

Query Match 79.2%; Score 570.5; DB 1; Length 238;
 Best Local Similarity 81.2%; Pred. No. 4.1e-35;
 Matches 112; Conservative 9; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFMIPVSGDVVMTOSPLSPYTPGEPASISCRSSOSLAKSYGNTYLSW 60
 Db 1 MKLPVRLV-LMFWIPASSSDVMTOSPLSPVSLGDASISCRSSKSLVHSHGNTYLSW 59
 QY 61 YLQKPGQSPQLLYIGISNRFSGVPDRFSGSGSGTDFTLKISRVEADPVGYYCLOGTHP 120
 Db 60 YLQKPGQSPKLLIKYVSNRFSGVPDRFSGSGSGTDFTLKISRVEADPGLGVYFCSGSTHP 119
 QY 121 YTFGQGTQVFIKRAADAP 138
 Db 120 PAFGGTKLEIKRAADAP 137

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